



SEQUENCE LISTING

<110> Barry, Gerard F.
Kishore, Ganesh M.
Padgette, Stephen R.
Stallings, William C.

<120> GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES

<130> 11899.0175.REUS07

<140> 10/622,201

<141> 2003-07-18

<150> US 08/306,063

<151> 1994-09-13

<150> US 07/749,611

<151> 1991-08-28

<150> US 07/576,537

<151> 1990-08-31

<160> 70

<170> PatentIn version 3.3

<210> 1

<211> 597

<212> DNA

<213> Figwort mosaic virus

<400> 1

```
tcatcaaaat atttagcagc attccagatt gggttcaatc aacaaggtac gagccatata 60
actttattca aattggtatc gccaaaacca agaaggaact cccatcctca aaggtttgta 120
aggaagaatt cttagtccaa agcctcaaca aggtcagggt acagagtctc caaaccatta 180
gccaaaagct acaggagatc aatgaagaat cttcaatcaa agtaaactac tgttccagca 240
catgcatcat ggtcagtaag tttagaaaa agacatccac cgaagactta aagttagtgg 300
gcatctttga aagtaatctt gtcaacatcg agcagctggc ttgtggggac cagacaaaaa 360
aggaatggtg cagaattggt aggcgcacct accaaaagca tctttgcctt tattgcaaag 420
ataaagcaga ttcctctagt acaagtgggg aacaaaataa cgtggaaaag agctgtcctg 480
acagcccact cactaatgcg tatgacgaac gcagtgcga ccacaaaaga attccctcta 540
tataagaagg cattcattcc catttgaagg atcatcagat actaaccaat atttctc 597
```

<210> 2
 <211> 1982
 <212> DNA
 <213> Agrobacterium sp.

 <220>
 <221> CDS
 <222> (62)..(1426)

 <400> 2
 aagcccgcgt tctctccggc gctccgcccg gagagccgtg gatagattaa ggaagacgcc 60

 c atg tcg cac ggt gca agc agc cgg ccc gca acc gcc cgc aaa tcc tct 109
 Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
 1 5 10 15

 ggc ctt tcc gga acc gtc cgc att ccc ggc gac aag tcg atc tcc cac 157
 Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
 20 25 30

 cgg tcc ttc atg ttc ggc ggt ctc gcg agc ggt gaa acg cgc atc acc 205
 Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
 35 40 45

 ggc ctt ctg gaa ggc gag gac gtc atc aat acg ggc aag gcc atg cag 253
 Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
 50 55 60

 gcc atg ggc gcc agg atc cgt aag gaa ggc gac acc tgg atc atc gat 301
 Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
 65 70 75 80

 ggc gtc ggc aat ggc ggc ctc ctg gcg cct gag gcg ccg ctc gat ttc 349
 Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
 85 90 95

 ggc aat gcc gcc acg ggc tgc cgc ctg acc atg ggc ctc gtc ggg gtc 397
 Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
 100 105 110

 tac gat ttc gac agc acc ttc atc ggc gac gcc tcg ctc aca aag cgc 445
 Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
 115 120 125

 ccg atg ggc cgc gtg ttg aac ccg ctg cgc gaa atg ggc gtg cag gtg 493
 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
 130 135 140

 aaa tcg gaa gac ggt gac cgt ctt ccc gtt acc ttg cgc ggg ccg aag 541
 Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
 145 150 155 160

 acg ccg acg ccg atc acc tac cgc gtg ccg atg gcc tcc gca cag gtg 589
 Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
 165 170 175

aag tcc gcc gtg ctg ctc gcc ggc ctc aac acg ccc ggc atc acg acg Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr	637
180 185 190	
gtc atc gag ccg atc atg acg cgc gat cat acg gaa aag atg ctg cag Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln	685
195 200 205	
ggc ttt ggc gcc aac ctt acc gtc gag acg gat gcg gac ggc gtg cgc Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg	733
210 215 220	
acc atc cgc ctg gaa ggc cgc ggc aag ctc acc ggc caa gtc atc gac Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp	781
225 230 235 240	
gtg ccg ggc gac ccg tcc tcg acg gcc ttc ccg ctg gtt gcg gcc ctg Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu	829
245 250 255	
ctt gtt ccg ggc tcc gac gtc acc atc ctc aac gtg ctg atg aac ccc Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro	877
260 265 270	
acc cgc acc ggc ctc atc ctg acg ctg cag gaa atg ggc gcc gac atc Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile	925
275 280 285	
gaa gtc atc aac ccg cgc ctt gcc ggc ggc gaa gac gtg gcg gac ctg Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu	973
290 295 300	
cgc gtt cgc tcc tcc acg ctg aag ggc gtc acg gtg ccg gaa gac cgc Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg	1021
305 310 315 320	
gcg cct tcg atg atc gac gaa tat ccg att ctc gct gtc gcc gcc gcc Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala	1069
325 330 335	
ttc gcg gaa ggg gcg acc gtg atg aac ggt ctg gaa gaa ctc cgc gtc Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val	1117
340 345 350	
aag gaa agc gac cgc ctc tcg gcc gtc gcc aat ggc ctc aag ctc aat Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn	1165
355 360 365	
ggc gtg gat tgc gat gag ggc gag acg tcg ctc gtc gtg cgc ggc cgc Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg	1213
370 375 380	
cct gac ggc aag ggg ctc ggc aac gcc tcg ggc gcc gcc gtc gcc acc Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr	1261
385 390 395 400	

cat ctc gat cac cgc atc gcc atg agc ttc ctc gtc atg ggc ctc gtg 1309
His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
405 410 415
tcg gaa aac cct gtc acg gtg gac gat gcc acg atg atc gcc acg agc 1357
Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
420 425 430
ttc ccg gag ttc atg gac ctg atg gcc ggg ctg ggc gcg aag atc gaa 1405
Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
435 440 445
ctc tcc gat acg aag gct gcc tgatgacctt cacaatcgcc atogatggtc 1456
Leu Ser Asp Thr Lys Ala Ala
450 455
ccgctgcggc cggcaagggg acgctctcgc gccgtatcgc ggaggtctat ggctttcatc 1516
atctcgatac gggcctgacc tatcgcgcca cggccaaagc gctgctcgat cgcggcctgt 1576
cgcttgatga cgaggcgggt gcggccgatg tcgcccgaat tctcgatctt gccgggctcg 1636
accggtcggg gctgtcggcc catgccatcg gcgaggcggc ttcgaagatc gcggtcatgc 1696
cctcgggtgcg gcgggcgctg gtcgaggcgc agcgcagctt tgcggcgcgt gagccgggca 1756
cgggtgctgga tggacgcgat atcggcacgg tggctctgcc ggatgcgccg gtgaagctct 1816
atgtcaccgc gtcaccgga gtcgcgcga aacgccgcta tgacgaaatc ctcggcaatg 1876
gcggggtggc cgattacggg acgatcctcg aggatatccg ccgccgcgac gagcgggaca 1936
tgggtcgggc ggacagtcct ttgaagcccg ccgacgatgc gcactt 1982

<210> 3
<211> 455
<212> PRT
<213> Agrobacterium sp.

<400> 3

Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
1 5 10 15
Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
20 25 30
Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
35 40 45
Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
50 55 60
Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
65 70 75 80

Gly	Val	Gly	Asn	Gly	Gly	Leu	Leu	Ala	Pro	Glu	Ala	Pro	Leu	Asp	Phe		
				85					90					95			
Gly	Asn	Ala	Ala	Thr	Gly	Cys	Arg	Leu	Thr	Met	Gly	Leu	Val	Gly	Val		
			100					105					110				
Tyr	Asp	Phe	Asp	Ser	Thr	Phe	Ile	Gly	Asp	Ala	Ser	Leu	Thr	Lys	Arg		
		115					120					125					
Pro	Met	Gly	Arg	Val	Leu	Asn	Pro	Leu	Arg	Glu	Met	Gly	Val	Gln	Val		
		130				135					140						
Lys	Ser	Glu	Asp	Gly	Asp	Arg	Leu	Pro	Val	Thr	Leu	Arg	Gly	Pro	Lys		
145					150					155					160		
Thr	Pro	Thr	Pro	Ile	Thr	Tyr	Arg	Val	Pro	Met	Ala	Ser	Ala	Gln	Val		
				165					170					175			
Lys	Ser	Ala	Val	Leu	Leu	Ala	Gly	Leu	Asn	Thr	Pro	Gly	Ile	Thr	Thr		
			180					185					190				
Val	Ile	Glu	Pro	Ile	Met	Thr	Arg	Asp	His	Thr	Glu	Lys	Met	Leu	Gln		
		195					200					205					
Gly	Phe	Gly	Ala	Asn	Leu	Thr	Val	Glu	Thr	Asp	Ala	Asp	Gly	Val	Arg		
	210					215					220						
Thr	Ile	Arg	Leu	Glu	Gly	Arg	Gly	Lys	Leu	Thr	Gly	Gln	Val	Ile	Asp		
225					230					235					240		
Val	Pro	Gly	Asp	Pro	Ser	Ser	Thr	Ala	Phe	Pro	Leu	Val	Ala	Ala	Leu		
				245					250					255			
Leu	Val	Pro	Gly	Ser	Asp	Val	Thr	Ile	Leu	Asn	Val	Leu	Met	Asn	Pro		
			260					265					270				
Thr	Arg	Thr	Gly	Leu	Ile	Leu	Thr	Leu	Gln	Glu	Met	Gly	Ala	Asp	Ile		
		275					280					285					
Glu	Val	Ile	Asn	Pro	Arg	Leu	Ala	Gly	Gly	Glu	Asp	Val	Ala	Asp	Leu		
	290					295					300						
Arg	Val	Arg	Ser	Ser	Thr	Leu	Lys	Gly	Val	Thr	Val	Pro	Glu	Asp	Arg		
305					310					315				320			
Ala	Pro	Ser	Met	Ile	Asp	Glu	Tyr	Pro	Ile	Leu	Ala	Val	Ala	Ala	Ala		
				325					330					335			
Phe	Ala	Glu	Gly	Ala	Thr	Val	Met	Asn	Gly	Leu	Glu	Glu	Leu	Arg	Val		
			340					345					350				
Lys	Glu	Ser	Asp	Arg	Leu	Ser	Ala	Val	Ala	Asn	Gly	Leu	Lys	Leu	Asn		
		355					360					365					
Gly	Val	Asp	Cys	Asp	Glu	Gly	Glu	Thr	Ser	Leu	Val	Val	Arg	Gly	Arg		
	370					375						380					

Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
 385 390 395 400

His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
 405 410 415

Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
 420 425 430

Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
 435 440 445

Leu Ser Asp Thr Lys Ala Ala
 450 455

<210> 4
 <211> 1673
 <212> DNA
 <213> Agrobacterium sp.

<220>
 <221> CDS
 <222> (86)..(1432)

<400> 4
 gtagccacac ataattacta tagctaggaa gcccgctatc tctcaatccc gcgtgatcgc 60

gccaaaatgt gactgtgaaa aatcc atg tcc cat tct gca tcc ccg aaa cca 112
 Met Ser His Ser Ala Ser Pro Lys Pro
 1 5

gca acc gcc cgc cgc tcg gag gca ctc acg ggc gaa atc cgc att ccg 160
 Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro
 10 15 20 25

ggc gac aag tcc atc tcg cat cgc tcc ttc atg ttt ggc ggt ctc gca 208
 Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala
 30 35 40

tcg ggc gaa acc cgc atc acc ggc ctt ctg gaa ggc gag gac gtc atc 256
 Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile
 45 50 55

aat aca ggc cgc gcc atg cag gcc atg ggc gcg aaa atc cgt aaa gag 304
 Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu
 60 65 70

ggc gat gtc tgg atc atc aac ggc gtc ggc aat ggc tgc ctg ttg cag 352
 Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln
 75 80 85

ccc gaa gct gcg ctc gat ttc ggc aat gcc gga acc ggc gcg cgc ctc 400
 Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu
 90 95 100 105

acc atg ggc ctt gtc ggc acc tat gac atg aag acc tcc ttt atc ggc	448
Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly	
110 115 120	
gac gcc tcg ctg tcg aag cgc ccg atg ggc cgc gtg ctg aac ccg ttg	496
Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu	
125 130 135	
cgc gaa atg ggc gtt cag gtg gaa gca gcc gat ggc gac cgc atg ccg	544
Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro	
140 145 150	
ctg acg ctg atc ggc ccg aag acg gcc aat ccg atc acc tat cgc gtg	592
Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr Arg Val	
155 160 165	
ccg atg gcc tcc gcg cag gta aaa tcc gcc gtg ctg ctc gcc ggt ctc	640
Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala Gly Leu	
170 175 180 185	
aac acg ccg ggc gtc acc acc gtc atc gag ccg gtc atg acc cgc gac	688
Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr Arg Asp	
190 195 200	
cac acc gaa aag atg ctg cag ggc ttt ggc gcc gac ctc acg gtc gag	736
His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr Val Glu	
205 210 215	
acc gac aag gat ggc gtg cgc cat atc cgc atc acc ggc cag ggc aag	784
Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln Gly Lys	
220 225 230	
ctt gtc ggc cag acc atc gac gtg ccg ggc gat ccg tca tcg acc gcc	832
Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser Thr Ala	
235 240 245	
ttc ccg ctc gtt gcc gcc ctt ctg gtg gaa ggt tcc gac gtc acc atc	880
Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val Thr Ile	
250 255 260 265	
cgc aac gtg ctg atg aac ccg acc cgt acc ggc ctc atc ctc acc ttg	928
Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu	
270 275 280	
cag gaa atg ggc gcc gat atc gaa gtg ctc aat gcc cgt ctt gca ggc	976
Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu Ala Gly	
285 290 295	
ggc gaa gac gtc gcc gat ctg cgc gtc agg gct tcg aag ctc aag ggc	1024
Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu Lys Gly	
300 305 310	
gtc gtc gtt ccg ccg gaa cgt gcg ccg tcg atg atc gac gaa tat ccg	1072
Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro	
315 320 325	

gtc ctg gcg att gcc gcc tcc ttc gcg gaa ggc gaa acc gtg atg gac	1120
Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val Met Asp	
330 335 340 345	
ggg ctc gac gaa ctg cgc gtc aag gaa tcg gat cgt ctg gca gcg gtc	1168
Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Val	
350 355 360	
gca cgc ggc ctt gaa gcc aac ggc gtc gat tgc acc gaa ggc gag atg	1216
Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly Glu Met	
365 370 375	
tcg ctg acg gtt cgc ggc cgc ccc gac ggc aag gga ctg ggc ggc ggc	1264
Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly Gly Gly	
380 385 390	
acg gtt gca acc cat ctc gat cat cgt atc gcg atg agc ttc ctc gtg	1312
Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val	
395 400 405	
atg ggc ctt gcg gcg gaa aag ccg gtg acg gtt gac gac agt aac atg	1360
Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser Asn Met	
410 415 420 425	
atc gcc acg tcc ttc ccc gaa ttc atg gac atg atg ccg gga ttg ggc	1408
Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly	
430 435 440	
gca aag atc gag ttg agc ata ctc tagtcactcg acagcgaaaa tattatttgc	1462
Ala Lys Ile Glu Leu Ser Ile Leu	
445	
gagattgggc attattaccg gttggtctca gcggggggttt aatgtccaat cttccatacg	1522
taacagcatc aggaaatata aaaaaagctt tagaaggaat tgctagagca gcgacgccgc	1582
ctaagctttc tcaagacttc gttaaaactg tactgaaatc ccgggggggtc cggggatcaa	1642
atgacttcat ttctgagaaa ttggcctcgc a	1673
<210> 5	
<211> 449	
<212> PRT	
<213> Agrobacterium sp.	
<400> 5	
Met Ser His Ser Ala Ser Pro Lys Pro Ala Thr Ala Arg Arg Ser Glu	
1 5 10 15	
Ala Leu Thr Gly Glu Ile Arg Ile Pro Gly Asp Lys Ser Ile Ser His	
20 25 30	
Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr	
35 40 45	

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Arg Ala Met Gln
 50 55 60
 Ala Met Gly Ala Lys Ile Arg Lys Glu Gly Asp Val Trp Ile Ile Asn
 65 70 75 80
 Gly Val Gly Asn Gly Cys Leu Leu Gln Pro Glu Ala Ala Leu Asp Phe
 85 90 95
 Gly Asn Ala Gly Thr Gly Ala Arg Leu Thr Met Gly Leu Val Gly Thr
 100 105 110
 Tyr Asp Met Lys Thr Ser Phe Ile Gly Asp Ala Ser Leu Ser Lys Arg
 115 120 125
 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
 130 135 140
 Glu Ala Ala Asp Gly Asp Arg Met Pro Leu Thr Leu Ile Gly Pro Lys
 145 150 155 160
 Thr Ala Asn Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
 165 170 175
 Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Val Thr Thr
 180 185 190
 Val Ile Glu Pro Val Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
 195 200 205
 Gly Phe Gly Ala Asp Leu Thr Val Glu Thr Asp Lys Asp Gly Val Arg
 210 215 220
 His Ile Arg Ile Thr Gly Gln Gly Lys Leu Val Gly Gln Thr Ile Asp
 225 230 235 240
 Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
 245 250 255
 Leu Val Glu Gly Ser Asp Val Thr Ile Arg Asn Val Leu Met Asn Pro
 260 265 270
 Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
 275 280 285
 Glu Val Leu Asn Ala Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
 290 295 300
 Arg Val Arg Ala Ser Lys Leu Lys Gly Val Val Val Pro Pro Glu Arg
 305 310 315 320
 Ala Pro Ser Met Ile Asp Glu Tyr Pro Val Leu Ala Ile Ala Ala Ser
 325 330 335
 Phe Ala Glu Gly Glu Thr Val Met Asp Gly Leu Asp Glu Leu Arg Val
 340 345 350

Lys Glu Ser Asp Arg Leu Ala Ala Val Ala Arg Gly Leu Glu Ala Asn
 355 360 365
 Gly Val Asp Cys Thr Glu Gly Glu Met Ser Leu Thr Val Arg Gly Arg
 370 375 380
 Pro Asp Gly Lys Gly Leu Gly Gly Gly Thr Val Ala Thr His Leu Asp
 385 390 395 400
 His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Ala Ala Glu Lys
 405 410 415
 Pro Val Thr Val Asp Asp Ser Asn Met Ile Ala Thr Ser Phe Pro Glu
 420 425 430
 Phe Met Asp Met Met Pro Gly Leu Gly Ala Lys Ile Glu Leu Ser Ile
 435 440 445
 Leu

<210> 6
 <211> 1500
 <212> DNA
 <213> Pseudomonas sp.

<220>
 <221> CDS
 <222> (34) .. (1380)

<400> 6
 gtgatcgcg caaaatgtga ctgtgaaaaa tcc atg tcc cat tct gca tcc ccg 54
 Met Ser His Ser Ala Ser Pro
 1 5
 aaa cca gca acc gcc cgc cgc tcg gag gca ctc acg ggc gaa atc cgc 102
 Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg
 10 15 20
 att ccg ggc gac aag tcc atc tcg cat cgc tcc ttc atg ttt ggc ggt 150
 Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly
 25 30 35
 ctc gca tcg ggc gaa acc cgc atc acc ggc ctt ctg gaa ggc gag gac 198
 Leu Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp
 40 45 50 55
 gtc atc aat aca ggc cgc gcc atg cag gcc atg ggc gcg aaa atc cgt 246
 Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg
 60 65 70
 aaa gag ggc gat gtc tgg atc atc aac ggc gtc ggc aat ggc tgc ctg 294
 Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu
 75 80 85

ttg cag ccc gaa gct gcg ctc gat ttc ggc aat gcc gga acc ggc gcg	342
Leu Gln Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala	
90 95 100	
cgc ctc acc atg ggc ctt gtc ggc acc tat gac atg aag acc tcc ttt	390
Arg Leu Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe	
105 110 115	
atc ggc gac gcc tcg ctg tcg aag cgc ccg atg ggc cgc gtg ctg aac	438
Ile Gly Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn	
120 125 130 135	
ccg ttg cgc gaa atg ggc gtt cag gtg gaa gca gcc gat ggc gac cgc	486
Pro Leu Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg	
140 145 150	
atg ccg ctg acg ctg atc ggc ccg aag acg gcc aat ccg atc acc tat	534
Met Pro Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr	
155 160 165	
cgc gtg ccg atg gcc tcc gcg cag gta aaa tcc gcc gtg ctg ctc gcc	582
Arg Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala	
170 175 180	
ggt ctc aac acg ccg ggc gtc acc acc gtc atc gag ccg gtc atg acc	630
Gly Leu Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr	
185 190 195	
cgc gac cac acc gaa aag atg ctg cag ggc ttt ggc gcc gac ctc acg	678
Arg Asp His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr	
200 205 210 215	
gtc gag acc gac aag gat ggc gtg cgc cat atc cgc atc acc ggc cag	726
Val Glu Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln	
220 225 230	
ggc aag ctt gtc ggc cag acc atc gac gtg ccg ggc gat ccg tca tcg	774
Gly Lys Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser	
235 240 245	
acc gcc ttc ccg ctc gtt gcc gcc ctt ctg gtg gaa ggt tcc gac gtc	822
Thr Ala Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val	
250 255 260	
acc atc cgc aac gtg ctg atg aac ccg acc cgt acc ggc ctc atc ctc	870
Thr Ile Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu	
265 270 275	
acc ttg cag gaa atg ggc gcc gat atc gaa gtg ctc aat gcc cgt ctt	918
Thr Leu Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu	
280 285 290 295	
gca ggc ggc gaa gac gtc gcc gat ctg cgc gtc agg gct tcg aag ctc	966
Ala Gly Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu	
300 305 310	

aag ggc gtc gtc gtt ccg ccg gaa cgt gcg ccg tcg atg atc gac gaa 1014
Lys Gly Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu
315 320 325

tat ccg gtc ctg gcg att gcc gcc tcc ttc gcg gaa ggc gaa acc gtg 1062
Tyr Pro Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val
330 335 340

atg gac ggg ctc gac gaa ctg cgc gtc aag gaa tcg gat cgt ctg gca 1110
Met Asp Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala
345 350 355

gcg gtc gca cgc ggc ctt gaa gcc aac ggc gtc gat tgc acc gaa ggc 1158
Ala Val Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly
360 365 370 375

gag atg tcg ctg acg gtt cgc ggc cgc ccc gac ggc aag gga ctg ggc 1206
Glu Met Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly
380 385 390

ggc ggc acg gtt gca acc cat ctc gat cat cgt atc gcg atg agc ttc 1254
Gly Gly Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe
395 400 405

ctc gtg atg ggc ctt gcg gcg gaa aag ccg gtg acg gtt gac gac agt 1302
Leu Val Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser
410 415 420

aac atg atc gcc acg tcc ttc ccc gaa ttc atg gac atg atg ccg gga 1350
Asn Met Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly
425 430 435

ttg ggc gca aag atc gag ttg agc ata ctc tagtcactcg acagcgaaaa 1400
Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu
440 445

tattatttgc gagattgggc attattaccg gttggtctca gcggggggttt aatgtccaat 1460

cttccatcacg taacagcatc aggaaatata aaaaaagctt 1500

<210> 7
<211> 449
<212> PRT
<213> *Pseudomonas* sp.

<400> 7

Met Ser His Ser Ala Ser Pro Lys Pro Ala Thr Ala Arg Arg Ser Glu
1 5 10 15

Ala Leu Thr Gly Glu Ile Arg Ile Pro Gly Asp Lys Ser Ile Ser His
20 25 30

Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
35 40 45

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Arg Ala Met Gln
 50 55 60
 Ala Met Gly Ala Lys Ile Arg Lys Glu Gly Asp Val Trp Ile Ile Asn
 65 70 75 80
 Gly Val Gly Asn Gly Cys Leu Leu Gln Pro Glu Ala Ala Leu Asp Phe
 85 90 95
 Gly Asn Ala Gly Thr Gly Ala Arg Leu Thr Met Gly Leu Val Gly Thr
 100 105 110
 Tyr Asp Met Lys Thr Ser Phe Ile Gly Asp Ala Ser Leu Ser Lys Arg
 115 120 125
 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
 130 135 140
 Glu Ala Ala Asp Gly Asp Arg Met Pro Leu Thr Leu Ile Gly Pro Lys
 145 150 155 160
 Thr Ala Asn Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
 165 170 175
 Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Val Thr Thr
 180 185 190
 Val Ile Glu Pro Val Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
 195 200 205
 Gly Phe Gly Ala Asp Leu Thr Val Glu Thr Asp Lys Asp Gly Val Arg
 210 215 220
 His Ile Arg Ile Thr Gly Gln Gly Lys Leu Val Gly Gln Thr Ile Asp
 225 230 235 240
 Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
 245 250 255
 Leu Val Glu Gly Ser Asp Val Thr Ile Arg Asn Val Leu Met Asn Pro
 260 265 270
 Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
 275 280 285
 Glu Val Leu Asn Ala Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
 290 295 300
 Arg Val Arg Ala Ser Lys Leu Lys Gly Val Val Val Pro Pro Glu Arg
 305 310 315 320
 Ala Pro Ser Met Ile Asp Glu Tyr Pro Val Leu Ala Ile Ala Ala Ser
 325 330 335
 Phe Ala Glu Gly Glu Thr Val Met Asp Gly Leu Asp Glu Leu Arg Val
 340 345 350

Lys Glu Ser Asp Arg Leu Ala Ala Val Ala Arg Gly Leu Glu Ala Asn
 355 360 365
 Gly Val Asp Cys Thr Glu Gly Glu Met Ser Leu Thr Val Arg Gly Arg
 370 375 380
 Pro Asp Gly Lys Gly Leu Gly Gly Gly Thr Val Ala Thr His Leu Asp
 385 390 395 400
 His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Ala Ala Glu Lys
 405 410 415
 Pro Val Thr Val Asp Asp Ser Asn Met Ile Ala Thr Ser Phe Pro Glu
 420 425 430
 Phe Met Asp Met Met Pro Gly Leu Gly Ala Lys Ile Glu Leu Ser Ile
 435 440 445

Leu

<210> 8
 <211> 423
 <212> PRT
 <213> Escherichia coli

<400> 8

Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Thr Ile Asn Leu
 1 5 10 15
 Pro Gly Ser Lys Thr Val Ser Asn Arg Ala Leu Leu Leu Ala Ala Leu
 20 25 30
 Ala His Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp Asp Val
 35 40 45
 Arg His Met Leu Asn Ala Leu Thr Ala Leu Gly Val Ser Tyr Thr Leu
 50 55 60
 Ser Ala Asp Arg Thr Arg Cys Glu Ile Ile Gly Asn Gly Gly Pro Leu
 65 70 75 80
 His Ala Glu Gly Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly Thr Ala
 85 90 95
 Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Ser Asn Asp Ile Val
 100 105 110
 Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His Leu Val
 115 120 125
 Asp Ala Leu Arg Leu Gly Gly Ala Lys Ile Thr Tyr Leu Glu Gln Glu
 130 135 140
 Asn Tyr Pro Pro Leu Arg Leu Gln Gly Gly Phe Thr Gly Gly Asn Val
 145 150 155 160

Asp Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu Leu Met
 165 170 175
 Thr Ala Pro Leu Ala Pro Glu Asp Thr Val Ile Arg Ile Lys Gly Asp
 180 185 190
 Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met Lys Thr
 195 200 205
 Phe Gly Val Glu Ile Glu Asn Gln His Tyr Gln Gln Phe Val Val Lys
 210 215 220
 Gly Gly Gln Ser Tyr Gln Ser Pro Gly Thr Tyr Leu Val Glu Gly Asp
 225 230 235 240
 Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Ala Ala Ile Lys Gly Gly
 245 250 255
 Thr Val Lys Val Thr Gly Ile Gly Arg Asn Ser Met Gln Gly Asp Ile
 260 265 270
 Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Ile Cys Trp Gly
 275 280 285
 Asp Asp Tyr Ile Ser Cys Thr Arg Gly Glu Leu Asn Ala Ile Asp Met
 290 295 300
 Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr Ala Ala
 305 310 315 320
 Leu Phe Ala Lys Gly Thr Thr Arg Leu Arg Asn Ile Tyr Asn Trp Arg
 325 330 335
 Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu Arg Lys
 340 345 350
 Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile Thr Pro
 355 360 365
 Pro Glu Lys Leu Asn Phe Ala Glu Ile Ala Thr Tyr Asn Asp His Arg
 370 375 380
 Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro Val Thr
 385 390 395 400
 Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr Phe Glu
 405 410 415
 Gln Leu Ala Arg Ile Ser Gln
 420

<210> 9
 <211> 1377
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

<400> 9
 ccatggctca cgggtgcaagc agccgtccag caactgctcg taagtccctct ggtctttctg 60
 gaaccgtccg tattccaggt gacaagtcta tctcccacag gtccttcatg tttggagggtc 120
 tcgctagcgg tgaaactcgt atcaccgggtc ttttggaagg tgaagatggt atcaacactg 180
 gtaaggctat gcaagctatg ggtgccagaa tccgtaagga aggtgatact tggatcattg 240
 atggtgttgg taacggtgga ctcttctgctc ctgagggtcc tctcgatttc ggtaacgctg 300
 caactggttg ccgtttgact atgggtcttg ttggtgttta cgatttcgat agcactttca 360
 ttggtgacgc ttctctcact aagcgtccaa tgggtcgtgt gttgaaccca cttcgcgaaa 420
 tgggtgtgca ggtgaagtct gaagacgggtg atcgtcttcc agttaccttg cgtggaccaa 480
 agactccaac gccaatcacc tacagggtac ctatggcttc cgctcaagtg aagtcgcgtg 540
 ttctgcttgc tgggtctcaac accccaggta tcaccactgt tatcgagcca atcatgactc 600
 gtgaccacac tgaaaagatg cttcaagggt ttggtgctaa ccttaccgtt gagactgatg 660
 ctgacgggtg gcgtaccatc cgtcttgaag gtcgtggtaa gctcaccggg caagtgattg 720
 atgttccagg tgatccatcc tctactgctt tcccattggg tgctgccttg cttgttccag 780
 gttccgacgt caccatcctt aacgttttga tgaacccaac ccgtactggg ctcatcttga 840
 ctctgcagga aatgggtgcc gacatcgaag tgatcaaccc acgtcttgct ggtggagaag 900
 acgtggctga cttgcgtgtt cgttcttcta ctttgaaggg tgttactgtt ccagaagacc 960
 gtgctccttc tatgatcgac gagtatccaa ttctcgctgt tgcagctgca ttcgctgaag 1020
 gtgctaccgt tatgaacggg ttggaagaac tccgtgttaa ggaaagcgac cgtctttctg 1080
 ctgtcgcaaa cgggtctcaag ctcaacgggtg ttgattgcca tgaagggtgag acttctctcg 1140
 tcgtgcgtgg tcgtcctgac ggtaagggtc tcggtaacgc ttctggagca gctgtcgcta 1200
 cccacctcga tcaccgtatc gctatgagct tcctcgttat ggggtctcgtt tctgaaaacc 1260
 ctgttactgt tgatgatgct actatgatcg ctactagctt ccagagttc atggatttga 1320
 tggtgtgtct tggagctaag atcgaactct ccgacactaa ggctgcttga tgagctc 1377

<210> 10
 <211> 318
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (87)..(317)

<400> 10
 agatctatcg ataagcttga tgtaattgga ggaagatcaa aattttcaat cccattctt 60
 cgattgcttc aattgaagtt tctccg atg gcg caa gtt agc aga atc tgc aat 113
 Met Ala Gln Val Ser Arg Ile Cys Asn
 1 5
 ggt gtg cag aac cca tct ctt atc tcc aat ctc tcg aaa tcc agt caa 161
 Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln
 10 15 20 25
 cgc aaa tct ccc tta tcg gtt tct ctg aag acg cag cag cat cca cga 209
 Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln Gln His Pro Arg
 30 35 40
 gct tat ccg att tcg tcg tcg tgg gga ttg aag aag agt ggg atg acg 257
 Ala Tyr Pro Ile Ser Ser Ser Trp Gly Leu Lys Lys Ser Gly Met Thr
 45 50 55
 tta att ggc tct gag ctt cgt cct ctt aag gtc atg tct tct gtt tcc 305
 Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Ser Val Ser
 60 65 70
 acg gcg tgc atg c 318
 Thr Ala Cys Met
 75

<210> 11
 <211> 77
 <212> PRT
 <213> Arabidopsis thaliana

<400> 11
 Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu
 1 5 10 15
 Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val
 20 25 30
 Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser
 35 40 45
 Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg
 50 55 60
 Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Cys Met
 65 70 75

<210> 12
 <211> 402
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (87)..(401)

<400> 12
 agatctatcg ataagcttga tgtaattgga ggaagatcaa aattttcaat cccattctt 60
 cgattgcttc aattgaagtt tctccg atg gcg caa gtt agc aga atc tgc aat 113
 Met Ala Gln Val Ser Arg Ile Cys Asn
 1 5
 ggt gtg cag aac cca tct ctt atc tcc aat ctc tcg aaa tcc agt caa 161
 Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln
 10 15 20 25
 cgc aaa tct ccc tta tcg gtt tct ctg aag acg cag cag cat cca cga 209
 Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln Gln His Pro Arg
 30 35 40
 gct tat ccg att tcg tcg tcg tgg gga ttg aag aag agt ggg atg acg 257
 Ala Tyr Pro Ile Ser Ser Ser Trp Gly Leu Lys Lys Ser Gly Met Thr
 45 50 55
 tta att ggc tct gag ctt cgt cct ctt aag gtc atg tct tct gtt tcc 305
 Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Ser Val Ser
 60 65 70
 acg gcg gag aaa gcg tcg gag att gta ctt caa ccc att aga gaa atc 353
 Thr Ala Glu Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile
 75 80 85
 tcc ggt ctt att aag ttg cct ggc tcc aag tct cta tca aat aga att c 402
 Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile
 90 95 100 105

<210> 13
 <211> 105
 <212> PRT
 <213> Arabidopsis thaliana

<400> 13
 Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu
 1 5 10 15
 Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val
 20 25 30
 Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser
 35 40 45

Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg
50 55 60

Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Glu Lys Ala Ser Glu
65 70 75 80

Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu Ile Lys Leu Pro
85 90 95

Gly Ser Lys Ser Leu Ser Asn Arg Ile
100 105

<210> 14
<211> 233
<212> DNA
<213> Petunia x hybrida

<220>
<221> CDS
<222> (14)..(232)

<400> 14
agatctttca aga atg gca caa att aac aac atg gct caa ggg ata caa 49
Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln
1 5 10

acc ctt aat ccc aat tcc aat ttc cat aaa ccc caa gtt cct aaa tct 97
Thr Leu Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser
15 20 25

tca agt ttt ctt gtt ttt gga tct aaa aaa ctg aaa aat tca gca aat 145
Ser Ser Phe Leu Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn
30 35 40

tct atg ttg gtt ttg aaa aaa gat tca att ttt atg caa aag ttt tgt 193
Ser Met Leu Val Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys
45 50 55 60

tcc ttt agg att tca gca tca gtg gct aca gcc tgc atg c 233
Ser Phe Arg Ile Ser Ala Ser Val Ala Thr Ala Cys Met
65 70

<210> 15
<211> 73
<212> PRT
<213> Petunia x hybrida

<400> 15
Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro
1 5 10 15

Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu
20 25 30

Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val
35 40 45

Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile
50 55 60

Ser Ala Ser Val Ala Thr Ala Cys Met
65 70

<210> 16
<211> 352
<212> DNA
<213> Petunia x hybrida

<220>
<221> CDS
<222> (49) .. (351)

<400> 16
agatctgcta gaaataattt tgtttaactt taagaaggag atatatcc atg gca caa 57
Met Ala Gln
1

att aac aac atg gct caa ggg ata caa acc ctt aat ccc aat tcc aat 105
Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro Asn Ser Asn
5 10 15

ttc cat aaa ccc caa gtt cct aaa tct tca agt ttt ctt gtt ttt gga 153
Phe His Lys Pro Gln Val Pro Lys Ser Ser Phe Leu Val Phe Gly
20 25 30 35

tct aaa aaa ctg aaa aat tca gca aat tct atg ttg gtt ttg aaa aaa 201
Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val Leu Lys Lys
40 45 50

gat tca att ttt atg caa aag ttt tgt tcc ttt agg att tca gca tca 249
Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile Ser Ala Ser
55 60 65

gtg gct aca gca cag aag cct tct gag ata gtg ttg caa ccc att aaa 297
Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys
70 75 80

gag att tca ggc act gtt aaa ttg cct ggc tct aaa tca tta tct aat 345
Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn
85 90 95

aga att c 352
Arg Ile
100

<210> 17
 <211> 101
 <212> PRT
 <213> Petunia x hybrida

<400> 17

Met	Ala	Gln	Ile	Asn	Asn	Met	Ala	Gln	Gly	Ile	Gln	Thr	Leu	Asn	Pro
1				5					10					15	
Asn	Ser	Asn	Phe	His	Lys	Pro	Gln	Val	Pro	Lys	Ser	Ser	Ser	Phe	Leu
			20					25					30		
Val	Phe	Gly	Ser	Lys	Lys	Leu	Lys	Asn	Ser	Ala	Asn	Ser	Met	Leu	Val
		35					40					45			
Leu	Lys	Lys	Asp	Ser	Ile	Phe	Met	Gln	Lys	Phe	Cys	Ser	Phe	Arg	Ile
	50					55					60				
Ser	Ala	Ser	Val	Ala	Thr	Ala	Gln	Lys	Pro	Ser	Glu	Ile	Val	Leu	Gln
65					70					75					80
Pro	Ile	Lys	Glu	Ile	Ser	Gly	Thr	Val	Lys	Leu	Pro	Gly	Ser	Lys	Ser
				85					90					95	
Leu	Ser	Asn	Arg	Ile											
				100											

<210> 18
 <211> 28
 <212> PRT
 <213> Agrobacterium sp.

<220>
 <221> UNSURE
 <222> (1)..(18)
 <223> Xaa = Unknown

<400> 18

Xaa	His	Gly	Ala	Ser	Ser	Arg	Pro	Ala	Thr	Ala	Arg	Lys	Ser	Ser	Gly
1				5					10					15	
Leu	Xaa	Gly	Thr	Val	Arg	Ile	Pro	Gly	Asp	Lys	Met				
			20					25							

<210> 19
 <211> 13
 <212> PRT
 <213> Agrobacterium sp.

<400> 19

Ala	Pro	Ser	Met	Ile	Asp	Glu	Tyr	Pro	Ile	Leu	Ala	Val
1				5					10			

<210> 20
 <211> 15
 <212> PRT
 <213> Agrobacterium sp.

<400> 20

Ile	Thr	Gly	Leu	Leu	Glu	Gly	Glu	Asp	Val	Ile	Asn	Thr	Gly	Lys
1			5						10					15

<210> 21
 <211> 17
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

<400> 21
 atgathgayg artaycc 17

<210> 22
 <211> 17
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (1)..(17)
 <223> R = A or G;
 Y = C or T/U;

N = A or C or G or T/U;

H = A or C or T/U

<400> 22
 gargaygtna thaacac 17

<210> 23
 <211> 17
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (1)..(17)
 <223> R = A or G;
 Y = C or T/U;

N = A or C or G or T/U;
H = A or C or T/U

<400> 23	
gargaygtna thaatac	17
<210> 24	
<211> 38	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Oligonucleotide	
<400> 24	
cgtggataga tctaggaaga caaccatggc tcacggtc	38
<210> 25	
<211> 44	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Oligonucleotide	
<400> 25	
ggatagatta aggaagacgc gcatgcttca cggtgcaagc agcc	44
<210> 26	
<211> 35	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Oligonucleotide	
<400> 26	
ggctgcctga tgagctccac aatcgccatc gatgg	35
<210> 27	
<211> 32	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Oligonucleotide	
<400> 27	
cgtcgctcgt cgtgcgtggc cgccctgacg gc	32
<210> 28	
<211> 29	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Oligonucleotide	

<400> 28
cgggcaaggc catgcaggct atgggcgcc 29

<210> 29
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 29
cgggctgccg cctgactatg ggcctcgtcg g 31

<210> 30
<211> 15
<212> PRT
<213> Pseudomonas sp.

<220>
<221> NON_CONS
<222> (1)..(1)
<223> Xaa = unknown

<400> 30
Xaa His Ser Ala Ser Pro Lys Pro Ala Thr Ala Arg Arg Ser Glu
1 5 10 15

<210> 31
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<220>
<221> misc_feature
<222> (1)..(17)
<223> B = C or G or T

S = G or C

Y = C or T

<400> 31
gcggtbgcsg gyttsgg 17

<210> 32
<211> 16
<212> PRT
<213> Artificial sequence

<220>
 <223> Synthetic
 <400> 32
 Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu
 1 5 10 15

<210> 33
 <211> 13
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Oligonucleotide

<400> 33

Leu Asp Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr
 1 5 10

<210> 34
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Oligonucleotide

<400> 34
 cggcaatgcc gccaccggcg cgcgcc 26

<210> 35
 <211> 49
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Oligonucleotide

<400> 35
 ggacggctgc ttgcaccgtg aagcatgctt aagcttggcg taatcatgg 49

<210> 36
 <211> 35
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Oligonucleotide

<400> 36
 ggaagacgcc cagaattcac ggtgcaagca gccggg 35

<210> 37
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> NON_CONS
<222> (2)..(2)
<223> Xaa = Gly, Ser, Thr, Cys, Tyr, Asn, Gln, Asp, or Glu

<220>
<221> NON_CONS
<222> (4)..(4)
<223> Xaa = Ser or Thr

<400> 37

Arg Xaa His Xaa Glu
1 5

<210> 38
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> NON_CONS
<222> (4)..(4)
<223> Xaa = Ser or Thr

<400> 38

Gly Asp Lys Xaa
1

<210> 39
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> NON_CONS
<222> (4)..(4)
<223> Xaa=Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val

<400> 39

Ser Ala Gln Xaa Lys
1 5

<210> 40
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> NON_CONS
<222> (2)..(2)
<223> Xaa=Ala, Arg, Asn, Asp, Cys, ln, lu, ly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val

<400> 40

Asn Xaa Thr Arg
1

<210> 41
<211> 1287
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1287)

<400> 41
atg aaa cga gat aag gtg cag acc tta cat gga gaa ata cat att ccc 48
Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro
1 5 10 15

ggt gat aaa tcc att tct cac cgc tct gtt atg ttt ggc gcg cta gcg 96
Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala
20 25 30

gca ggc aca aca aca gtt aaa aac ttt ctg ccg gga gca gat tgt ctg 144
Ala Gly Thr Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu
35 40 45

agc acg atc gat tgc ttt aga aaa atg ggt gtt cac att gag caa agc 192
Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser
50 55 60

agc agc gat gtc gtg att cac gga aaa gga atc gat gcc ctg aaa gag 240
Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu
65 70 75 80

cca gaa agc ctt tta gat gtc gga aat tca ggt aca acg att cgc ctg 288
Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu
85 90 95

atg ctc gga ata ttg gcg ggc cgt cct ttt tac agc gcg gta gcc gga Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly 100 105 110	336
gat gag agc att gcg aaa cgc cca atg aag cgt gtg act gag cct ttg Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu 115 120 125	384
aaa aaa atg ggg gct aaa atc gac ggc aga gcc ggc gga gag ttt aca Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr 130 135 140	432
ccg ctg tca gtg agc ggc gct tca tta aaa gga att gat tat gta tca Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser 145 150 155 160	480
cct gtt gca agc gcg caa att aaa tct gct gtt ttg ctg gcc gga tta Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu 165 170 175	528
cag gct gag ggc aca aca act gta aca gag ccc cat aaa tct cgg gac Gln Ala Glu Gly Thr Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp 180 185 190	576
cac act gag cgg atg ctt tct gct ttt ggc gtt aag ctt tct gaa gat His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp 195 200 205	624
caa acg agt gtt tcc att gct ggt ggc cag aaa ctg aca gct gct gat Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp 210 215 220	672
att ttt gtt cct gga gac att tct tca gcc gcg ttt ttc ctt gct gct Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala 225 230 235 240	720
ggc gcg atg gtt cca aac agc aga att gta ttg aaa aac gta ggt tta Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu 245 250 255	768
aat ccg act cgg aca ggt att att gat gtc ctt caa aac atg ggg gca Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala 260 265 270	816
aaa ctt gaa atc aaa cca tct gct gat agc ggt gca gag cct tat gga Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly 275 280 285	864
gat ttg att ata gaa acg tca tct cta aag gca gtt gaa atc gga gga Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly 290 295 300	912
gat atc att ccg cgt tta att gat gag atc cct atc atc gcg ctt ctt Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu 305 310 315 320	960

gcg act cag gcg gaa gga acc acc gtt att aag gac gcg gca gag cta	1008
Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu	
325 330 335	
aaa gtg aaa gaa aca aac cgt att gat act gtt gtt tct gag ctt cgc	1056
Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Val Ser Glu Leu Arg	
340 345 350	
aag ctg ggt gct gaa att gaa ccg aca gca gat gga atg aag gtt tat	1104
Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr	
355 360 365	
ggc aaa caa acg ttg aaa ggc ggc gct gca gtg tcc agc cac gga gat	1152
Gly Lys Gln Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp	
370 375 380	
cat cga atc gga atg atg ctt ggt att gct tcc tgt ata acg gag gag	1200
His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu	
385 390 395 400	
ccg att gaa atc gag cac acg gat gcc att cac gtt tct tat cca acc	1248
Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr	
405 410 415	
ttc ttc gag cat tta aat aag ctt tcg aaa aaa tcc tga	1287
Phe Phe Glu His Leu Asn Lys Leu Ser Lys Lys Ser	
420 425	
<210> 42	
<211> 428	
<212> PRT	
<213> Bacillus subtilis	
<400> 42	
Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro	
1 5 10 15	
Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala	
20 25 30	
Ala Gly Thr Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu	
35 40 45	
Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser	
50 55 60	
Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu	
65 70 75 80	
Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu	
85 90 95	
Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly	
100 105 110	

Asp	Glu	Ser	Ile	Ala	Lys	Arg	Pro	Met	Lys	Arg	Val	Thr	Glu	Pro	Leu	115	120	125
Lys	Lys	Met	Gly	Ala	Lys	Ile	Asp	Gly	Arg	Ala	Gly	Gly	Glu	Phe	Thr	130	135	140
Pro	Leu	Ser	Val	Ser	Gly	Ala	Ser	Leu	Lys	Gly	Ile	Asp	Tyr	Val	Ser	145	150	155
Pro	Val	Ala	Ser	Ala	Gln	Ile	Lys	Ser	Ala	Val	Leu	Leu	Ala	Gly	Leu	165	170	175
Gln	Ala	Glu	Gly	Thr	Thr	Thr	Val	Thr	Glu	Pro	His	Lys	Ser	Arg	Asp	180	185	190
His	Thr	Glu	Arg	Met	Leu	Ser	Ala	Phe	Gly	Val	Lys	Leu	Ser	Glu	Asp	195	200	205
Gln	Thr	Ser	Val	Ser	Ile	Ala	Gly	Gly	Gln	Lys	Leu	Thr	Ala	Ala	Asp	210	215	220
Ile	Phe	Val	Pro	Gly	Asp	Ile	Ser	Ser	Ala	Ala	Phe	Phe	Leu	Ala	Ala	225	230	235
Gly	Ala	Met	Val	Pro	Asn	Ser	Arg	Ile	Val	Leu	Lys	Asn	Val	Gly	Leu	245	250	255
Asn	Pro	Thr	Arg	Thr	Gly	Ile	Ile	Asp	Val	Leu	Gln	Asn	Met	Gly	Ala	260	265	270
Lys	Leu	Glu	Ile	Lys	Pro	Ser	Ala	Asp	Ser	Gly	Ala	Glu	Pro	Tyr	Gly	275	280	285
Asp	Leu	Ile	Ile	Glu	Thr	Ser	Ser	Leu	Lys	Ala	Val	Glu	Ile	Gly	Gly	290	295	300
Asp	Ile	Ile	Pro	Arg	Leu	Ile	Asp	Glu	Ile	Pro	Ile	Ile	Ala	Leu	Leu	305	310	315
Ala	Thr	Gln	Ala	Glu	Gly	Thr	Thr	Val	Ile	Lys	Asp	Ala	Ala	Glu	Leu	325	330	335
Lys	Val	Lys	Glu	Thr	Asn	Arg	Ile	Asp	Thr	Val	Val	Ser	Glu	Leu	Arg	340	345	350
Lys	Leu	Gly	Ala	Glu	Ile	Glu	Pro	Thr	Ala	Asp	Gly	Met	Lys	Val	Tyr	355	360	365
Gly	Lys	Gln	Thr	Leu	Lys	Gly	Gly	Ala	Ala	Val	Ser	Ser	His	Gly	Asp	370	375	380
His	Arg	Ile	Gly	Met	Met	Leu	Gly	Ile	Ala	Ser	Cys	Ile	Thr	Glu	Glu	385	390	395
Pro	Ile	Glu	Ile	Glu	His	Thr	Asp	Ala	Ile	His	Val	Ser	Tyr	Pro	Thr	405	410	415

Phe Phe Glu His Leu Asn Lys Leu Ser Lys Lys Ser
420 425

<210> 43
<211> 1293
<212> DNA
<213> Staphylococcus aureus

<220>
<221> CDS
<222> (1)..(1293)

<400> 43
atg gta aat gaa caa atc att gat att tca ggt ccg tta aag ggc gaa 48
Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu
1 5 10 15

ata gaa gtg ccg ggc gat aag tca atg aca cac cgt gca atc atg ttg 96
Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu
20 25 30

gcg tcg cta gct gaa ggt gta tct act ata tat aag cca cta ctt ggc 144
Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly
35 40 45

gaa gat tgt cgt cgt acg atg gac att ttc cga cac tta ggt gta gaa 192
Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu
50 55 60

atc aaa gaa gat gat gaa aaa tta gtt gtg act tcc cca gga tat caa 240
Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln
65 70 75 80

gtt aac acg cca cat caa gta ttg tat aca ggt aat tct ggt acg aca 288
Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr
85 90 95

aca cga tta ttg gca ggt ttg tta agt ggt tta ggt aat gaa agt gtt 336
Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val
100 105 110

ttg tct ggc gat gtt tca att ggt aaa agg cca atg gat cgt gtc ttg 384
Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu
115 120 125

aga cca ttg aaa ctt atg gat gcg aat att gaa ggt att gaa gat aat 432
Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn
130 135 140

tat aca cca tta att att aag cca tct gtc ata aaa ggt ata aat tat 480
Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr
145 150 155 160

caa atg gaa gtt gca agt gca caa gta aaa agt gcc att tta ttt gca 528
Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala
165 170 175

agt ttg ttt tct aag gaa ccg acc atc att aaa gaa tta gat gta agt	576
Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser	
180 185 190	
cga aat cat act gag acg atg ttc aaa cat ttt aat att cca att gaa	624
Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu	
195 200 205	
gca gaa ggg tta tca att aat aca acc cct gaa gca att cga tac att	672
Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile	
210 215 220	
aaa cct gca gat ttt cat gtt cct ggc gat att tca tct gca gcg ttc	720
Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe	
225 230 235 240	
ttt att gtt gca gca ctt atc aca cca gga agt gat gta aca att cat	768
Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His	
245 250 255	
aat gtt gga atc aat caa aca cgt tca ggt att att gat att gtt gaa	816
Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu	
260 265 270	
aaa atg ggc ggt aat atc caa ctt ttc aat caa aca act ggt gct gaa	864
Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu	
275 280 285	
cct act gct tct att cgt att caa tac aca cca atg ctt caa cca ata	912
Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile	
290 295 300	
aca atc gaa gga gaa tta gtt cca aaa gca att gat gaa ctg cct gta	960
Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val	
305 310 315 320	
ata gca tta ctt tgt aca caa gca gtt ggc acg agt aca att aaa gat	1008
Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp	
325 330 335	
gcc gag gaa tta aaa gta aaa gaa aca aat aga att gat aca acg gct	1056
Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala	
340 345 350	
gat atg tta aac ttg tta ggg ttt gaa tta caa cca act aat gat gga	1104
Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly	
355 360 365	
ttg att att cat ccg tca gaa ttt aaa aca aat gca aca gat att tta	1152
Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu	
370 375 380	
act gat cat cga ata gga atg atg ctt gca gtt gct tgt gta ctt tca	1200
Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser	
385 390 395 400	

agc gag cct gtc aaa atc aaa caa ttt gat gct gta aat gta tca ttt 1248
 Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe
 405 410 415

cca gga ttt tta cca aaa cta aag ctt tta caa aat gag gga taa 1293
 Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly
 420 425 430

<210> 44
 <211> 430
 <212> PRT
 <213> Staphylococcus aureus

<400> 44

Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu
 1 5 10 15

Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu
 20 25 30

Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly
 35 40 45

Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu
 50 55 60

Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln
 65 70 75 80

Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr
 85 90 95

Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val
 100 105 110

Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu
 115 120 125

Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn
 130 135 140

Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr
 145 150 155 160

Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala
 165 170 175

Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser
 180 185 190

Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu
 195 200 205

Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile
 210 215 220

Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe
 225 230 235 240
 Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His
 245 250 255
 Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu
 260 265 270
 Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu
 275 280 285
 Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile
 290 295 300
 Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val
 305 310 315 320
 Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp
 325 330 335
 Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala
 340 345 350
 Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly
 355 360 365
 Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu
 370 375 380
 Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser
 385 390 395 400
 Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe
 405 410 415
 Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly
 420 425 430

<210> 45
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Oligonucleotide

<400> 45
 ggaacatatg aaacgagata aggtgcag

28

<210> 46
 <211> 35
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Oligonucleotide

<400> 46
ggaattcaaa cttcaggatc ttgagataga aaatg 35

<210> 47
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 47
ggggccatgg taaatgaaca aatcattg 28

<210> 48
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 48
gggggagctc attatccctc attttgtaaa agc 33

<210> 49
<211> 480
<212> PRT
<213> Saccharomyces cerevisiae

<400> 49

Leu Thr Asp Glu Thr Leu Val Tyr Pro Phe Lys Asp Ile Pro Ala Asp
1 5 10 15

Gln Gln Lys Val Val Ile Pro Pro Gly Ser Lys Ser Ile Ser Asn Arg
20 25 30

Ala Leu Ile Leu Ala Ala Leu Gly Glu Gly Gln Cys Lys Ile Lys Asn
35 40 45

Leu Leu His Ser Asp Asp Thr Lys His Met Leu Thr Ala Val His Glu
50 55 60

Leu Lys Gly Ala Thr Ile Ser Trp Glu Asp Asn Gly Glu Thr Val Val
65 70 75 80

Val Glu Gly His Gly Gly Ser Thr Leu Ser Ala Cys Ala Asp Pro Leu
85 90 95

Tyr Leu Gly Asn Ala Gly Thr Ala Ser Arg Phe Leu Thr Ser Leu Ala
100 105 110

Ala Leu Val Asn Ser Thr Ser Ser Gln Lys Tyr Ile Val Leu Thr Gly
115 120 125

Asn Ala Arg Met Gln Gln Arg Pro Ile Ala Pro Leu Val Asp Ser Leu
 130 135 140
 Arg Ala Asn Gly Thr Lys Ile Glu Tyr Leu Asn Asn Glu Gly Ser Leu
 145 150 155 160
 Pro Ile Lys Val Tyr Thr Asp Ser Val Phe Lys Gly Gly Arg Ile Glu
 165 170 175
 Leu Ala Ala Thr Val Ser Ser Gln Tyr Val Ser Ser Ile Leu Met Cys
 180 185 190
 Ala Pro Tyr Ala Glu Glu Pro Val Thr Leu Ala Leu Val Gly Gly Lys
 195 200 205
 Pro Ile Ser Lys Leu Tyr Val Asp Met Thr Ile Lys Met Met Glu Lys
 210 215 220
 Phe Gly Ile Asn Val Glu Thr Ser Thr Thr Glu Pro Tyr Thr Tyr Tyr
 225 230 235 240
 Ile Pro Lys Gly His Tyr Ile Asn Pro Ser Glu Tyr Val Ile Glu Ser
 245 250 255
 Asp Ala Ser Ser Ala Thr Tyr Pro Leu Ala Phe Ala Ala Met Thr Gly
 260 265 270
 Thr Thr Val Thr Val Pro Asn Ile Gly Phe Glu Ser Leu Gln Gly Asp
 275 280 285
 Ala Arg Phe Ala Arg Asp Val Leu Lys Pro Met Gly Cys Lys Ile Thr
 290 295 300
 Gln Thr Ala Thr Ser Thr Thr Val Ser Gly Pro Pro Val Gly Thr Leu
 305 310 315 320
 Lys Pro Leu Lys His Val Asp Met Glu Pro Met Thr Asp Ala Phe Leu
 325 330 335
 Thr Ala Cys Val Val Ala Ala Ile Ser His Asp Ser Asp Pro Asn Ser
 340 345 350
 Ala Asn Thr Thr Thr Ile Glu Gly Ile Ala Asn Gln Arg Val Lys Glu
 355 360 365
 Cys Asn Arg Ile Leu Ala Met Ala Thr Glu Leu Ala Lys Phe Gly Val
 370 375 380
 Lys Thr Thr Glu Leu Pro Asp Gly Ile Gln Val His Gly Leu Asn Ser
 385 390 395 400
 Ile Lys Asp Leu Lys Val Pro Ser Asp Ser Ser Gly Pro Val Gly Val
 405 410 415
 Cys Thr Tyr Asp Asp His Arg Val Ala Met Ser Phe Ser Leu Leu Ala
 420 425 430

Gly Met Val Asn Ser Gln Asn Glu Arg Asp Glu Val Ala Asn Pro Val
435 440 445

Arg Ile Leu Glu Arg His Cys Thr Gly Lys Thr Trp Pro Gly Trp Trp
450 455 460

Asp Val Leu His Ser Glu Leu Gly Ala Lys Leu Asp Gly Ala Glu Pro
465 470 475 480

<210> 50
<211> 460
<212> PRT
<213> Aspergillus nidulans

<400> 50

Leu Ala Pro Ser Ile Glu Val His Pro Gly Val Ala His Ser Ser Asn
1 5 10 15

Val Ile Cys Ala Pro Pro Gly Ser Lys Ser Ile Ser Asn Arg Ala Leu
20 25 30

Val Leu Ala Ala Leu Gly Ser Gly Thr Cys Arg Ile Lys Asn Leu Leu
35 40 45

His Ser Asp Asp Thr Glu Val Met Leu Asn Ala Leu Glu Arg Leu Gly
50 55 60

Ala Ala Thr Phe Ser Trp Glu Glu Glu Gly Glu Val Leu Val Val Asn
65 70 75 80

Gly Lys Gly Gly Asn Leu Gln Ala Ser Ser Ser Pro Leu Tyr Leu Gly
85 90 95

Asn Ala Gly Thr Ala Ser Arg Phe Leu Thr Thr Val Ala Thr Leu Ala
100 105 110

Asn Ser Ser Thr Val Asp Ser Ser Val Leu Thr Gly Asn Asn Arg Met
115 120 125

Lys Gln Arg Pro Ile Gly Asp Leu Val Asp Ala Leu Thr Ala Asn Val
130 135 140

Leu Pro Leu Asn Thr Ser Lys Gly Arg Ala Ser Leu Pro Leu Lys Ile
145 150 155 160

Ala Ala Ser Gly Gly Phe Ala Gly Gly Asn Ile Asn Leu Ala Ala Lys
165 170 175

Val Ser Ser Gln Tyr Val Ser Ser Leu Leu Met Cys Ala Pro Tyr Ala
180 185 190

Lys Glu Pro Val Thr Leu Arg Leu Val Gly Gly Lys Pro Ile Ser Gln
195 200 205

Pro Tyr Ile Asp Met Thr Thr Ala Met Met Arg Ser Phe Gly Ile Asp
210 215 220

Val	Gln	Lys	Ser	Thr	Thr	Glu	Glu	His	Thr	Tyr	His	Ile	Pro	Gln	Gly	225	230	235	240
Arg	Tyr	Val	Asn	Pro	Ala	Glu	Tyr	Val	Ile	Glu	Ser	Asp	Ala	Ser	Cys	245	250	255	
Ala	Thr	Tyr	Pro	Leu	Ala	Val	Ala	Ala	Val	Thr	Gly	Thr	Thr	Cys	Thr	260	265	270	
Val	Pro	Asn	Ile	Gly	Ser	Ala	Ser	Leu	Gln	Gly	Asp	Ala	Arg	Phe	Ala	275	280	285	
Val	Glu	Val	Leu	Arg	Pro	Met	Gly	Cys	Thr	Val	Glu	Gln	Thr	Glu	Thr	290	295	300	
Ser	Thr	Thr	Val	Thr	Gly	Pro	Ser	Asp	Gly	Ile	Leu	Arg	Ala	Thr	Ser	305	310	315	320
Lys	Arg	Gly	Tyr	Gly	Thr	Asn	Asp	Arg	Cys	Val	Pro	Arg	Cys	Phe	Arg	325	330	335	
Thr	Gly	Ser	His	Arg	Pro	Met	Glu	Lys	Ser	Gln	Thr	Thr	Pro	Pro	Val	340	345	350	
Ser	Ser	Gly	Ile	Ala	Asn	Gln	Arg	Val	Lys	Glu	Cys	Asn	Arg	Ile	Lys	355	360	365	
Ala	Met	Lys	Asp	Glu	Leu	Ala	Lys	Phe	Gly	Val	Ile	Cys	Arg	Glu	His	370	375	380	
Asp	Asp	Gly	Leu	Glu	Ile	Asp	Gly	Ile	Asp	Arg	Ser	Asn	Leu	Arg	Gln	385	390	395	400
Pro	Val	Gly	Gly	Val	Phe	Cys	Tyr	Asp	Asp	His	Arg	Val	Ala	Phe	Ser	405	410	415	
Phe	Ser	Val	Leu	Ser	Leu	Val	Thr	Pro	Gln	Pro	Thr	Leu	Ile	Leu	Glu	420	425	430	
Lys	Glu	Cys	Val	Gly	Lys	Thr	Trp	Pro	Gly	Trp	Trp	Asp	Thr	Leu	Arg	435	440	445	
Gln	Leu	Phe	Lys	Val	Lys	Leu	Glu	Gly	Lys	Glu	Leu					450	455	460	
<210> 51																			
<211> 444																			
<212> PRT																			
<213> Brassica napus																			
<400> 51																			
Lys	Ala	Ser	Glu	Ile	Val	Leu	Gln	Pro	Ile	Arg	Glu	Ile	Ser	Gly	Leu	1	5	10	15

Ile	Lys	Leu	Pro	Gly	Ser	Lys	Ser	Leu	Ser	Asn	Arg	Ile	Leu	Leu	Leu	20	25	30
Ala	Ala	Leu	Ser	Glu	Gly	Thr	Thr	Val	Val	Asp	Asn	Leu	Leu	Asn	Ser	35	40	45
Asp	Asp	Ile	Asn	Tyr	Met	Leu	Asp	Ala	Leu	Lys	Lys	Leu	Gly	Leu	Asn	50	55	60
Val	Glu	Arg	Asp	Ser	Val	Asn	Asn	Arg	Ala	Val	Val	Glu	Gly	Cys	Gly	65	70	75
Gly	Ile	Phe	Pro	Ala	Ser	Leu	Asp	Ser	Lys	Ser	Asp	Ile	Glu	Leu	Tyr	85	90	95
Leu	Gly	Asn	Ala	Gly	Thr	Ala	Met	Arg	Pro	Leu	Thr	Ala	Ala	Val	Thr	100	105	110
Ala	Ala	Gly	Gly	Asn	Ala	Ser	Tyr	Val	Leu	Asp	Gly	Val	Pro	Arg	Met	115	120	125
Arg	Glu	Arg	Pro	Ile	Gly	Asp	Leu	Val	Val	Gly	Leu	Lys	Gln	Leu	Gly	130	135	140
Ala	Asp	Val	Glu	Cys	Thr	Leu	Gly	Thr	Asn	Cys	Pro	Pro	Val	Arg	Val	145	150	155
Asn	Ala	Asn	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser	165	170	175
Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala	180	185	190
Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Ile	Asp	Lys	Leu	Ile	Ser	Val	Pro	195	200	205
Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Val	Ser	Ala	210	215	220
Glu	His	Ser	Asp	Ser	Trp	Asp	Arg	Phe	Phe	Val	Lys	Gly	Gly	Gln	Lys	225	230	235
Tyr	Lys	Ser	Pro	Gly	Asn	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	245	250	255
Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Ile	Thr	Gly	Glu	Thr	Val	Thr	Val	260	265	270
Glu	Gly	Cys	Gly	Thr	Thr	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu	275	280	285
Val	Leu	Glu	Lys	Met	Gly	Cys	Lys	Val	Ser	Trp	Thr	Glu	Asn	Ser	Val	290	295	300
Thr	Val	Thr	Gly	Pro	Ser	Arg	Asp	Ala	Phe	Gly	Met	Arg	His	Leu	Arg	305	310	315

Ala Val Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
 325 330 335
 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
 340 345 350
 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
 355 360 365
 Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Ser Asp Tyr Cys
 370 375 380
 Val Ile Thr Pro Pro Ala Lys Val Lys Pro Ala Glu Ile Asp Thr Tyr
 385 390 395 400
 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
 405 410 415
 Val Pro Val Thr Ile Lys Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430
 Asp Tyr Phe Gln Val Leu Glu Ser Ile Thr Lys His
 435 440
 <210> 52
 <211> 444
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 52
 Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu
 1 5 10 15
 Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
 20 25 30
 Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn Ser
 35 40 45
 Asp Asp Ile Asn Tyr Met Leu Asp Ala Leu Lys Arg Leu Gly Leu Asn
 50 55 60
 Val Glu Thr Asp Ser Glu Asn Asn Arg Ala Val Val Glu Gly Cys Gly
 65 70 75 80
 Gly Ile Phe Pro Ala Ser Ile Asp Ser Lys Ser Asp Ile Glu Leu Tyr
 85 90 95
 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
 100 105 110
 Ala Ala Gly Gly Asn Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met
 115 120 125
 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
 130 135 140

Ala	Asp	Val	Glu	Cys	Thr	Leu	Gly	Thr	Asn	Cys	Pro	Pro	Val	Arg	Val	145	150	155	160
Asn	Ala	Asn	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser	165	170	175	
Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ser	Ala	Pro	Leu	Ala	180	185	190	
Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Val	Asp	Lys	Leu	Ile	Ser	Val	Pro	195	200	205	
Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Val	Ser	Val	210	215	220	
Glu	His	Ser	Asp	Ser	Trp	Asp	Arg	Phe	Phe	Val	Lys	Gly	Gly	Gln	Lys	225	230	235	240
Tyr	Lys	Ser	Pro	Gly	Asn	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	245	250	255	
Cys	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Ile	Thr	Gly	Glu	Thr	Val	Thr	Val	260	265	270	
Glu	Gly	Cys	Gly	Thr	Thr	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu	275	280	285	
Val	Leu	Glu	Lys	Met	Gly	Cys	Lys	Val	Ser	Trp	Thr	Glu	Asn	Ser	Val	290	295	300	
Thr	Val	Thr	Gly	Pro	Pro	Arg	Asp	Ala	Phe	Gly	Met	Arg	His	Leu	Arg	305	310	315	320
Ala	Ile	Asp	Val	Asn	Met	Asn	Lys	Met	Pro	Asp	Val	Ala	Met	Thr	Leu	325	330	335	
Ala	Val	Val	Ala	Leu	Phe	Ala	Asp	Gly	Pro	Thr	Thr	Ile	Arg	Asp	Val	340	345	350	
Ala	Ser	Trp	Arg	Val	Lys	Glu	Thr	Glu	Arg	Met	Ile	Ala	Ile	Cys	Thr	355	360	365	
Glu	Leu	Arg	Lys	Leu	Gly	Ala	Thr	Val	Glu	Glu	Gly	Ser	Asp	Tyr	Cys	370	375	380	
Val	Ile	Thr	Pro	Pro	Lys	Lys	Val	Lys	Thr	Ala	Glu	Ile	Asp	Thr	Tyr	385	390	395	400
Asp	Asp	His	Arg	Met	Ala	Met	Ala	Phe	Ser	Leu	Ala	Ala	Cys	Ala	Asp	405	410	415	
Val	Pro	Ile	Thr	Ile	Asn	Asp	Ser	Gly	Cys	Thr	Arg	Lys	Thr	Phe	Pro	420	425	430	
Asp	Tyr	Phe	Gln	Val	Leu	Glu	Arg	Ile	Thr	Lys	His					435	440		

<210> 53
 <211> 444
 <212> PRT
 <213> Nicotiana tabacum

<400> 53

Lys	Pro	Asn	Glu	Ile	Val	Leu	Gln	Pro	Ile	Lys	Asp	Ile	Ser	Gly	Thr	1	5	10	15
Val	Lys	Leu	Pro	Gly	Ser	Lys	Ser	Leu	Ser	Asn	Arg	Ile	Leu	Leu	Leu	20	25	30	
Ala	Ala	Leu	Ser	Lys	Gly	Arg	Thr	Val	Val	Asp	Asn	Leu	Leu	Ser	Ser	35	40	45	
Asp	Asp	Ile	His	Tyr	Met	Leu	Gly	Ala	Leu	Lys	Thr	Leu	Gly	Leu	His	50	55	60	
Val	Glu	Asp	Asp	Asn	Glu	Asn	Gln	Arg	Ala	Ile	Val	Glu	Gly	Cys	Gly	65	70	75	80
Gly	Gln	Phe	Pro	Val	Gly	Lys	Lys	Ser	Glu	Glu	Glu	Ile	Gln	Leu	Phe	85	90	95	
Leu	Gly	Asn	Ala	Gly	Thr	Ala	Met	Arg	Pro	Leu	Thr	Ala	Ala	Val	Thr	100	105	110	
Val	Ala	Gly	Gly	His	Ser	Arg	Tyr	Val	Leu	Asp	Gly	Val	Pro	Arg	Met	115	120	125	
Arg	Glu	Arg	Pro	Ile	Gly	Asp	Leu	Val	Asp	Gly	Leu	Lys	Gln	Leu	Gly	130	135	140	
Ala	Glu	Val	Asp	Cys	Phe	Leu	Gly	Thr	Asn	Cys	Pro	Pro	Val	Arg	Ile	145	150	155	160
Val	Ser	Lys	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser	165	170	175	
Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala	180	185	190	
Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Ile	Asp	Lys	Leu	Ile	Ser	Val	Pro	195	200	205	
Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Val	Ser	Val	210	215	220	
Glu	His	Thr	Ser	Ser	Trp	Asp	Lys	Phe	Leu	Val	Arg	Gly	Gly	Gln	Lys	225	230	235	240
Tyr	Lys	Ser	Pro	Gly	Lys	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	245	250	255	
Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Val	Thr	Gly	Gly	Thr	Val	Thr	Val	260	265	270	

Glu Gly Cys Gly Thr Ser Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
 275 280 285
 Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
 290 295 300
 Thr Val Lys Gly Pro Pro Arg Asn Ser Ser Gly Met Lys His Leu Arg
 305 310 315 320
 Ala Val Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
 325 330 335
 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
 340 345 350
 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
 355 360 365
 Glu Leu Arg Lys Leu Gly Ala Thr Val Val Glu Gly Ser Asp Tyr Cys
 370 375 380
 Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Glu Ile Asp Thr Tyr
 385 390 395 400
 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
 405 410 415
 Val Pro Val Thr Ile Lys Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430
 Asn Tyr Phe Asp Val Leu Gln Gln Tyr Ser Lys His
 435 440

<210> 54
 <211> 444
 <212> PRT
 <213> Lycopersicon esculentum

<220>
 <221> UNSURE
 <222> (1)..(444)
 <223> Xaa = any

<400> 54

Lys Pro His Glu Ile Val Leu Xaa Pro Ile Lys Asp Ile Ser Gly Thr
 1 5 10 15
 Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
 20 25 30
 Ala Ala Leu Ser Glu Gly Arg Thr Val Val Asp Asn Leu Leu Ser Ser
 35 40 45
 Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
 50 55 60

Glu Leu Arg Lys Leu Gly Ala Thr Val Val Glu Gly Ser Asp Tyr Cys
 370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Glu Ile Asp Thr Tyr
 385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
 405 410 415

Val Pro Val Thr Ile Lys Asn Pro Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430

Asp Tyr Phe Glu Val Leu Gln Lys Tyr Ser Lys His
 435 440

<210> 55
 <211> 444
 <212> PRT
 <213> Petunia x hybrida

<400> 55

Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly Thr
 1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
 20 25 30

Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Ser Ser
 35 40 45

Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
 50 55 60

Val Glu Glu Asp Ser Ala Asn Gln Arg Ala Val Val Glu Gly Cys Gly
 65 70 75 80

Gly Leu Phe Pro Val Gly Lys Glu Ser Lys Glu Glu Ile Gln Leu Phe
 85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
 100 105 110

Val Ala Gly Gly Asn Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
 115 120 125

Arg Glu Arg Pro Ile Ser Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
 130 135 140

Ala Glu Val Asp Cys Phe Leu Gly Thr Lys Cys Pro Pro Val Arg Ile
 145 150 155 160

Val Ser Lys Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
 165 170 175

Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala	180	185	190	
Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Ile	Asp	Lys	Leu	Ile	Ser	Val	Pro	195	200	205	
Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Ile	Ser	Val	210	215	220	
Glu	His	Ser	Ser	Ser	Trp	Asp	Arg	Phe	Phe	Val	Arg	Gly	Gly	Gln	Lys	225	230	235	240
Tyr	Lys	Ser	Pro	Gly	Lys	Ala	Phe	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	245	250	255	
Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Val	Thr	Gly	Gly	Thr	Ile	Thr	Val	260	265	270	
Glu	Gly	Cys	Gly	Thr	Asn	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu	275	280	285	
Val	Leu	Glu	Lys	Met	Gly	Ala	Glu	Val	Thr	Trp	Thr	Glu	Asn	Ser	Val	290	295	300	
Thr	Val	Lys	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Gly	Arg	Lys	His	Leu	Arg	305	310	315	320
Ala	Ile	Asp	Val	Asn	Met	Asn	Lys	Met	Pro	Asp	Val	Ala	Met	Thr	Leu	325	330	335	
Ala	Val	Val	Ala	Leu	Tyr	Ala	Asp	Gly	Pro	Thr	Ala	Ile	Arg	Asp	Val	340	345	350	
Ala	Ser	Trp	Arg	Val	Lys	Glu	Thr	Glu	Arg	Met	Ile	Ala	Ile	Cys	Thr	355	360	365	
Glu	Leu	Arg	Lys	Leu	Gly	Ala	Thr	Val	Glu	Glu	Gly	Pro	Asp	Tyr	Cys	370	375	380	
Ile	Ile	Thr	Pro	Pro	Glu	Lys	Leu	Asn	Val	Thr	Asp	Ile	Asp	Thr	Tyr	385	390	395	400
Asp	Asp	His	Arg	Met	Ala	Met	Ala	Phe	Ser	Leu	Ala	Ala	Cys	Ala	Asp	405	410	415	
Val	Pro	Val	Thr	Ile	Asn	Asp	Pro	Gly	Cys	Thr	Arg	Lys	Thr	Phe	Pro	420	425	430	
Asn	Tyr	Phe	Asp	Val	Leu	Gln	Gln	Tyr	Ser	Lys	His	435	440						

<210> 56
 <211> 444
 <212> PRT
 <213> Zea mays

<400> 56

Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
 1 5 10 15
 Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu
 20 25 30
 Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
 35 40 45
 Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
 50 55 60
 Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
 65 70 75 80
 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
 85 90 95
 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
 100 105 110
 Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
 115 120 125
 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
 130 135 140
 Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
 145 150 155 160
 Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
 165 170 175
 Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Pro
 180 185 190
 Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
 195 200 205
 Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
 210 215 220
 Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
 225 230 235 240
 Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
 245 250 255
 Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
 260 265 270
 Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
 275 280 285
 Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
 290 295 300

Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
 305 310 315 320
 Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
 325 330 335
 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
 340 345 350
 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
 355 360 365
 Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
 370 375 380
 Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
 385 390 395 400
 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
 405 410 415
 Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430
 Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
 435 440

<210> 57
 <211> 427
 <212> PRT
 <213> Salmonella gallinarum

<400> 57

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
 1 5 10 15
 Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
 20 25 30
 Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
 35 40 45
 Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
 50 55 60
 Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
 65 70 75 80
 Pro Leu Arg Ala Pro Gly Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly
 85 90 95
 Thr Ala Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Gln Asn Glu
 100 105 110

Ile	Val	Leu	Thr	Gly	Glu	Pro	Arg	Met	Lys	Glu	Arg	Pro	Ile	Gly	His	115	120	125	
Leu	Val	Asp	Ser	Leu	Arg	Gln	Gly	Gly	Ala	Asn	Ile	Asp	Tyr	Leu	Glu	130	135	140	
Gln	Glu	Asn	Tyr	Pro	Pro	Leu	Arg	Leu	Arg	Gly	Gly	Phe	Ile	Gly	Gly	145	150	155	160
Asp	Ile	Glu	Val	Asp	Gly	Ser	Val	Ser	Ser	Gln	Phe	Leu	Thr	Ala	Leu	165	170	175	
Leu	Met	Thr	Ala	Pro	Leu	Ala	Pro	Lys	Asp	Thr	Ile	Ile	Arg	Val	Lys	180	185	190	
Gly	Glu	Leu	Val	Ser	Lys	Pro	Tyr	Ile	Asp	Ile	Thr	Leu	Asn	Leu	Met	195	200	205	
Lys	Thr	Phe	Gly	Val	Glu	Ile	Ala	Asn	His	His	Tyr	Gln	Gln	Phe	Val	210	215	220	
Val	Lys	Gly	Gly	Gln	Gln	Tyr	His	Ser	Pro	Gly	Arg	Tyr	Leu	Val	Glu	225	230	235	240
Gly	Asp	Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala	Ala	Gly	Ala	Ile	Lys	245	250	255	
Gly	Gly	Thr	Val	Lys	Val	Thr	Gly	Ile	Gly	Arg	Lys	Ser	Met	Gln	Gly	260	265	270	
Asp	Ile	Arg	Phe	Ala	Asp	Val	Leu	Glu	Lys	Met	Gly	Ala	Thr	Ile	Thr	275	280	285	
Trp	Gly	Asp	Asp	Phe	Ile	Ala	Cys	Thr	Arg	Gly	Glu	Leu	His	Ala	Ile	290	295	300	
Asp	Met	Asp	Met	Asn	His	Ile	Pro	Asp	Ala	Ala	Met	Thr	Ile	Ala	Thr	305	310	315	320
Thr	Ala	Leu	Phe	Ala	Lys	Gly	Thr	Thr	Thr	Leu	Arg	Asn	Ile	Tyr	Asn	325	330	335	
Trp	Arg	Val	Lys	Glu	Thr	Asp	Arg	Leu	Phe	Ala	Met	Ala	Thr	Glu	Leu	340	345	350	
Arg	Lys	Val	Gly	Ala	Glu	Val	Glu	Glu	Gly	His	Asp	Tyr	Ile	Arg	Ile	355	360	365	
Thr	Pro	Pro	Ala	Lys	Leu	Gln	His	Ala	Asp	Ile	Gly	Thr	Tyr	Asn	Asp	370	375	380	
His	Arg	Met	Ala	Met	Cys	Phe	Ser	Leu	Val	Ala	Leu	Ser	Asp	Thr	Pro	385	390	395	400
Val	Thr	Ile	Leu	Asp	Pro	Lys	Cys	Thr	Ala	Lys	Thr	Phe	Pro	Asp	Tyr	405	410	415	

Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
420 425

<210> 58
<211> 427
<212> PRT
<213> Salmonella typhimurium

<400> 58

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
20 25 30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
65 70 75 80

Pro Leu Arg Ala Ser Gly Thr Leu Glu Leu Phe Leu Gly Asn Ala Gly
85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Gln Asn Glu
100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
145 150 155 160

Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175

Leu Met Thr Ala Pro Leu Ala Pro Glu Asp Thr Ile Ile Arg Val Lys
180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
195 200 205

Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
210 215 220

Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Gly Ile Lys
245 250 255

Gly Gly Thr Val Lys Val Thr Gly Ile Gly Gly Lys Ser Met Gln Gly
 260 265 270
 Asp Ile Arg Phe Ala Asp Val Leu His Lys Met Gly Ala Thr Ile Thr
 275 280 285
 Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
 290 295 300
 Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
 305 310 315 320
 Thr Ala Leu Phe Ala Lys Gly Thr Thr Thr Leu Arg Asn Ile Tyr Asn
 325 330 335
 Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
 340 345 350
 Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
 355 360 365
 Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
 370 375 380
 His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400
 Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415
 Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
 420 425

<210> 59
 <211> 427
 <212> PRT
 <213> *Klebsiella pneumoniae*

<400> 59

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Thr Val
 1 5 10 15
 Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
 20 25 30
 Ala Leu Ala Arg Gly Thr Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
 35 40 45
 Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Val His Tyr
 50 55 60
 Val Leu Ser Ser Asp Arg Thr Arg Cys Glu Val Thr Gly Thr Gly Gly
 65 70 75 80

Pro Leu Gln Ala Gly Ser Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly
 85 90 95
 Thr Ala Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Ser Asn Asp
 100 105 110
 Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
 115 120 125
 Leu Val Asp Ala Leu Arg Gln Gly Gly Ala Gln Ile Asp Tyr Leu Glu
 130 135 140
 Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Thr Gly Gly
 145 150 155 160
 Asp Val Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
 165 170 175
 Leu Met Ala Ser Pro Leu Ala Pro Gln Asp Thr Val Ile Ala Ile Lys
 180 185 190
 Gly Glu Leu Val Ser Arg Pro Tyr Ile Asp Ile Thr Leu His Leu Met
 195 200 205
 Lys Thr Phe Gly Val Glu Val Glu Asn Gln Ala Tyr Gln Arg Phe Ile
 210 215 220
 Val Arg Gly Asn Gln Gln Tyr Gln Ser Pro Gly Asp Tyr Leu Val Glu
 225 230 235 240
 Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile Lys
 245 250 255
 Gly Gly Thr Val Lys Val Thr Gly Ile Gly Arg Asn Ser Val Gln Gly
 260 265 270
 Asp Ile Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Val Thr
 275 280 285
 Trp Gly Glu Asp Tyr Ile Ala Cys Thr Arg Gly Glu Leu Asn Ala Ile
 290 295 300
 Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
 305 310 315 320
 Ala Ala Leu Phe Ala Arg Gly Thr Thr Thr Leu Arg Asn Ile Tyr Asn
 325 330 335
 Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
 340 345 350
 Arg Lys Val Gly Ala Glu Val Glu Glu Gly Glu Asp Tyr Ile Arg Ile
 355 360 365
 Thr Pro Pro Leu Thr Leu Gln Phe Ala Glu Ile Gly Thr Tyr Asn Asp
 370 375 380

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400

Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415

Phe Gly Gln Leu Ala Arg Ile Ser Thr Leu Ala
 420 425

<210> 60
 <211> 427
 <212> PRT
 <213> Yersinia enterocolitica

<400> 60

Met Leu Glu Ser Leu Thr Leu His Pro Ile Ala Leu Ile Asn Gly Thr
 1 5 10 15

Val Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu
 20 25 30

Ala Ala Leu Ala Glu Gly Thr Thr Gln Leu Asn Asn Leu Leu Asp Ser
 35 40 45

Asp Asp Ile Arg His Met Leu Asn Ala Leu Gln Ala Leu Gly Val Lys
 50 55 60

Tyr Arg Leu Ser Ala Asp Arg Thr Arg Cys Glu Val Asp Gly Leu Gly
 65 70 75 80

Gly Lys Leu Val Ala Glu Gln Pro Leu Glu Leu Phe Leu Gly Asn Ala
 85 90 95

Gly Thr Ala Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Lys Asn
 100 105 110

Asp Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly
 115 120 125

His Leu Val Asp Ala Leu Arg Gln Gly Gly Ala Gln Ile Asp Tyr Leu
 130 135 140

Glu Gln Glu Asn Tyr Arg Arg Cys Ile Ala Gly Gly Phe Arg Gly Gly
 145 150 155 160

Lys Leu Thr Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
 165 170 175

Leu Met Thr Ala Pro Leu Ala Glu Gln Asp Thr Glu Ile Gln Ile Gln
 180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu His Leu Met
 195 200 205

Lys Ala Phe Gly Val Asp Val Val His Glu Asn Tyr Gln Ile Phe His
 210 215 220

Ile Lys Gly Gly Gln Thr Tyr Arg Ser Pro Gly Ile Tyr Leu Val Glu
 225 230 235 240
 Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Ala Ala Ile Lys
 245 250 255
 Gly Gly Thr Val Arg Val Thr Gly Ile Gly Lys Gln Ser Val Gln Gly
 260 265 270
 Asp Thr Lys Phe Ala Asp Val Leu Glu Lys Met Gly Ala Lys Ile Ser
 275 280 285
 Trp Gly Asp Asp Tyr Ile Glu Cys Ser Arg Gly Glu Leu Gln Gly Ile
 290 295 300
 Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
 305 310 315 320
 Thr Ala Leu Phe Ala Asp Gly Pro Thr Val Ile Arg Asn Ile Tyr Asn
 325 330 335
 Trp Arg Val Lys Glu Thr Asp Arg Leu Ser Ala Met Ala Thr Glu Leu
 340 345 350
 Arg Lys Val Gly Ala Glu Val Glu Glu Gly Gln Asp Tyr Ile Arg Val
 355 360 365
 Val Pro Pro Ala Gln Leu Ile Ala Ala Glu Ile Gly Thr Tyr Asn Asp
 370 375 380
 His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400
 Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415
 Phe Glu Gln Leu Ala Arg Leu Ser Gln Ile Ala
 420 425

<210> 61
 <211> 432
 <212> PRT
 <213> Haemophilus influenzae

<400> 61

Met Glu Lys Ile Thr Leu Ala Pro Ile Ser Ala Val Glu Gly Thr Ile
 1 5 10 15
 Asn Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ala Leu Leu Leu Ala
 20 25 30
 Ala Leu Ala Lys Gly Thr Thr Lys Val Thr Asn Leu Leu Asp Ser Asp
 35 40 45

Asp Ile Arg His Met Leu Asn Ala Leu Lys Ala Leu Gly Val Arg Tyr
 50 55 60
 Gln Leu Ser Asp Asp Lys Thr Ile Cys Glu Ile Glu Gly Leu Gly Gly
 65 70 75 80
 Ala Phe Asn Ile Gln Asp Asn Leu Ser Leu Phe Leu Gly Asn Ala Gly
 85 90 95
 Thr Ala Met Arg Pro Leu Thr Ala Ala Leu Cys Leu Lys Gly Asn His
 100 105 110
 Glu Val Glu Ile Ile Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro
 115 120 125
 Ile Leu His Leu Val Asp Ala Leu Arg Gln Ala Gly Ala Asp Ile Arg
 130 135 140
 Tyr Leu Glu Asn Glu Gly Tyr Pro Pro Leu Ala Ile Arg Asn Lys Gly
 145 150 155 160
 Ile Lys Gly Gly Lys Val Lys Ile Asp Gly Ser Ile Ser Ser Gln Phe
 165 170 175
 Leu Thr Ala Leu Leu Met Ser Ala Pro Leu Ala Glu Asn Asp Thr Glu
 180 185 190
 Ile Glu Ile Ile Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr
 195 200 205
 Leu Ala Met Met Arg Asp Phe Gly Val Lys Val Glu Asn His His Tyr
 210 215 220
 Gln Lys Phe Gln Val Lys Gly Asn Gln Ser Tyr Ile Ser Pro Asn Lys
 225 230 235 240
 Tyr Leu Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala
 245 250 255
 Gly Ala Ile Lys Gly Lys Val Lys Val Thr Gly Ile Gly Lys Asn Ser
 260 265 270
 Ile Gln Gly Asp Arg Leu Phe Ala Asp Val Leu Glu Lys Met Gly Ala
 275 280 285
 Lys Ile Thr Trp Gly Glu Asp Phe Ile Gln Ala Glu His Ala Glu Leu
 290 295 300
 Asn Gly Ile Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr
 305 310 315 320
 Ile Ala Thr Thr Ala Leu Phe Ser Asn Gly Glu Thr Val Ile Arg Asn
 325 330 335
 Ile Tyr Asn Trp Arg Val Lys Glu Thr Asp Arg Leu Thr Ala Met Ala
 340 345 350

Thr Glu Leu Arg Lys Val Gly Ala Glu Val Glu Glu Gly Glu Asp Phe
 355 360 365

Ile Arg Ile Gln Pro Leu Ala Leu Asn Gln Phe Lys His Ala Asn Ile
 370 375 380

Glu Thr Tyr Asn Asp His Arg Met Ala Met Cys Phe Ser Leu Ile Ala
 385 390 395 400

Leu Ser Asn Thr Pro Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys
 405 410 415

Thr Phe Pro Thr Phe Phe Asn Glu Phe Glu Lys Ile Cys Leu Lys Asn
 420 425 430

<210> 62
 <211> 441
 <212> PRT
 <213> Pasteurella multocida

<400> 62

Val Ile Lys Asp Ala Thr Ala Ile Thr Leu Asn Pro Ile Ser Tyr Ile
 1 5 10 15

Glu Gly Glu Val Arg Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ala
 20 25 30

Leu Leu Leu Ser Ala Leu Ala Lys Gly Lys Thr Thr Leu Thr Asn Leu
 35 40 45

Leu Asp Ser Asp Asp Val Arg His Met Leu Asn Ala Leu Lys Glu Leu
 50 55 60

Gly Val Thr Tyr Gln Leu Ser Glu Asp Lys Ser Val Cys Glu Ile Glu
 65 70 75 80

Gly Leu Gly Arg Ala Phe Glu Trp Gln Ser Gly Leu Ala Leu Phe Leu
 85 90 95

Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Leu Cys Leu
 100 105 110

Ser Thr Pro Asn Arg Glu Gly Lys Asn Glu Ile Val Leu Thr Gly Glu
 115 120 125

Pro Arg Met Lys Glu Arg Pro Ile Gln His Leu Val Asp Ala Leu Cys
 130 135 140

Gln Ala Gly Ala Glu Ile Gln Tyr Leu Glu Gln Glu Gly Tyr Pro Pro
 145 150 155 160

Ile Ala Ile Arg Asn Thr Gly Leu Lys Gly Gly Arg Ile Gln Ile Asp
 165 170 175

Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu Leu Met Ala Ala Pro
 180 185 190

Met	Ala	Glu	Ala	Asp	Thr	Glu	Ile	Glu	Ile	Ile	Gly	Glu	Leu	Val	Ser		
		195					200					205					
Lys	Pro	Tyr	Ile	Asp	Ile	Thr	Leu	Lys	Met	Met	Gln	Thr	Phe	Gly	Val		
		210				215					220						
Glu	Val	Glu	Asn	Gln	Ala	Tyr	Gln	Arg	Phe	Leu	Val	Lys	Gly	His	Gln		
225					230					235					240		
Gln	Tyr	Gln	Ser	Pro	His	Arg	Phe	Leu	Val	Glu	Gly	Asp	Ala	Ser	Ser		
				245					250						255		
Ala	Ser	Tyr	Phe	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Gly	Lys	Val	Lys	Val		
			260					265						270			
Thr	Gly	Val	Gly	Lys	Asn	Ser	Ile	Gln	Gly	Asp	Arg	Leu	Phe	Ala	Asp		
		275					280						285				
Val	Leu	Glu	Lys	Met	Gly	Ala	His	Ile	Thr	Trp	Gly	Asp	Asp	Phe	Ile		
	290					295					300						
Gln	Val	Glu	Lys	Gly	Asn	Leu	Lys	Gly	Ile	Asp	Met	Asp	Met	Asn	His		
305					310					315					320		
Ile	Pro	Asp	Ala	Ala	Met	Thr	Ile	Ala	Thr	Thr	Ala	Leu	Phe	Ala	Glu		
				325					330					335			
Gly	Glu	Thr	Val	Ile	Arg	Asn	Ile	Tyr	Asn	Trp	Arg	Val	Lys	Glu	Thr		
			340					345					350				
Asp	Arg	Leu	Thr	Ala	Met	Ala	Thr	Glu	Leu	Arg	Lys	Val	Gly	Ala	Glu		
		355					360					365					
Val	Glu	Glu	Gly	Glu	Asp	Phe	Ile	Arg	Ile	Gln	Pro	Leu	Asn	Leu	Ala		
	370					375					380						
Gln	Phe	Gln	His	Ala	Glu	Leu	Asn	Ile	His	Asp	His	Arg	Met	Ala	Met		
385					390					395					400		
Cys	Phe	Ala	Leu	Ile	Ala	Leu	Ser	Lys	Thr	Ser	Val	Thr	Ile	Leu	Asp		
				405					410					415			
Pro	Ser	Cys	Thr	Ala	Lys	Thr	Phe	Pro	Thr	Phe	Leu	Ile	Leu	Phe	Thr		
			420					425					430				
Leu	Asn	Thr	Arg	Glu	Val	Ala	Tyr	Arg									
		435					440										

<210> 63
 <211> 426
 <212> PRT
 <213> Aeromonas salmonicida

<400> 63

Asn	Ser	Leu	Arg	Leu	Glu	Pro	Ile	Ser	Arg	Val	Ala	Gly	Glu	Val	Asn
1				5				10					15		
Leu	Pro	Gly	Ser	Lys	Ser	Val	Ser	Asn	Arg	Ala	Leu	Leu	Leu	Ala	Ala
			20					25					30		
Leu	Ala	Arg	Gly	Thr	Thr	Arg	Leu	Thr	Asn	Leu	Leu	Asp	Ser	Asp	Asp
		35					40					45			
Ile	Arg	His	Met	Leu	Ala	Ala	Leu	Thr	Gln	Leu	Gly	Val	Lys	Tyr	Lys
	50					55					60				
Leu	Ser	Ala	Asp	Lys	Thr	Glu	Cys	Thr	Val	His	Gly	Leu	Gly	Arg	Ser
65				70						75					80
Phe	Ala	Val	Ser	Ala	Pro	Val	Asn	Leu	Phe	Leu	Gly	Asn	Ala	Gly	Thr
				85				90						95	
Ala	Met	Arg	Pro	Leu	Cys	Ala	Ala	Leu	Cys	Leu	Gly	Ser	Gly	Glu	Tyr
			100					105					110		
Met	Leu	Gly	Gly	Glu	Pro	Arg	Met	Glu	Glu	Arg	Pro	Ile	Gly	His	Leu
		115					120					125			
Val	Asp	Cys	Leu	Ala	Leu	Lys	Gly	Ala	His	Ile	Gln	Tyr	Leu	Lys	Lys
	130					135					140				
Asp	Gly	Tyr	Pro	Pro	Leu	Val	Val	Asp	Ala	Lys	Gly	Leu	Trp	Gly	Gly
145					150					155					160
Asp	Val	His	Val	Asp	Gly	Ser	Val	Ser	Ser	Gln	Phe	Leu	Thr	Ala	Phe
				165				170						175	
Leu	Met	Ala	Ala	Pro	Ala	Met	Ala	Pro	Val	Ile	Pro	Arg	Ile	His	Ile
			180					185					190		
Lys	Gly	Glu	Leu	Val	Ser	Lys	Pro	Tyr	Ile	Asp	Ile	Thr	Leu	His	Ile
		195					200					205			
Met	Asn	Ser	Ser	Gly	Val	Val	Ile	Glu	His	Asp	Asn	Tyr	Lys	Leu	Phe
	210					215					220				
Tyr	Ile	Lys	Gly	Asn	Gln	Ser	Ile	Val	Ser	Pro	Gly	Asp	Phe	Leu	Val
225					230					235					240
Glu	Gly	Asp	Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala	Ala	Gly	Ala	Ile
				245					250					255	
Lys	Gly	Lys	Val	Arg	Val	Thr	Gly	Ile	Gly	Lys	His	Ser	Ile	Gly	Asp
			260					265					270		

Ile His Phe Ala Asp Val Leu Glu Arg Met Gly Ala Arg Ile Thr Trp
 275 280 285
 Gly Asp Asp Phe Ile Glu Ala Glu Gln Gly Pro Leu His Gly Val Asp
 290 295 300
 Met Asp Met Asn His Ile Pro Asp Val Gly His Asp His Ser Gly Gln
 305 310 315 320
 Ser His Cys Leu Pro Arg Val Pro Pro His Ser Gln His Leu Gln Leu
 325 330 335
 Ala Val Arg Asp Asp Arg Cys Thr Pro Cys Thr His Gly His Arg Arg
 340 345 350
 Ala Gln Ala Gly Val Ser Glu Glu Gly Thr Thr Phe Ile Thr Arg Asp
 355 360 365
 Ala Ala Asp Pro Ala Gln Ala Arg Arg Asp Arg His Leu Gln Arg Ser
 370 375 380
 Arg Ile Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Ile Ala Val
 385 390 395 400
 Thr Ile Asn Asp Pro Gly Cys Thr Ser Lys Thr Phe Pro Asp Tyr Phe
 405 410 415
 Asp Lys Leu Ala Ser Val Ser Gln Ala Val
 420 425

<210> 64
 <211> 442
 <212> PRT
 <213> Bacillus pertussis

<400> 64

Met Ser Gly Leu Ala Tyr Leu Asp Leu Pro Ala Ala Arg Leu Ala Arg
 1 5 10 15
 Gly Glu Val Ala Leu Pro Gly Ser Lys Ser Ile Ser Asn Arg Val Leu
 20 25 30
 Leu Leu Ala Ala Leu Ala Glu Gly Ser Thr Glu Ile Thr Gly Leu Leu
 35 40 45
 Asp Ser Asp Asp Thr Arg Val Met Leu Ala Ala Leu Arg Gln Leu Gly
 50 55 60
 Val Ser Val Gly Glu Val Ala Asp Gly Cys Val Thr Ile Glu Gly Val
 65 70 75 80
 Ala Arg Phe Pro Thr Glu Gln Ala Glu Leu Phe Leu Gly Asn Ala Gly
 85 90 95

Thr	Ala	Phe	Arg	Pro	Leu	Thr	Ala	Ala	Leu	Ala	Leu	Met	Gly	Gly	Asp	100	105	110	
Tyr	Arg	Leu	Ser	Gly	Val	Pro	Arg	Met	His	Glu	Arg	Pro	Ile	Gly	Asp	115	120	125	
Leu	Val	Asp	Ala	Leu	Arg	Gln	Phe	Gly	Ala	Gly	Ile	Glu	Tyr	Leu	Gly	130	135	140	
Gln	Ala	Gly	Tyr	Pro	Pro	Leu	Arg	Ile	Gly	Gly	Gly	Ser	Ile	Arg	Val	145	150	155	160
Asp	Gly	Pro	Val	Arg	Val	Glu	Gly	Ser	Val	Ser	Ser	Gln	Phe	Leu	Thr	165	170	175	
Ala	Leu	Leu	Met	Ala	Ala	Pro	Val	Leu	Ala	Arg	Arg	Ser	Gly	Gln	Asp	180	185	190	
Ile	Thr	Ile	Glu	Val	Val	Gly	Glu	Leu	Ile	Ser	Lys	Pro	Tyr	Ile	Glu	195	200	205	
Ile	Thr	Leu	Asn	Leu	Met	Ala	Arg	Phe	Gly	Val	Ser	Val	Arg	Arg	Asp	210	215	220	
Gly	Trp	Arg	Ala	Phe	Thr	Ile	Ala	Arg	Asp	Ala	Val	Tyr	Arg	Gly	Pro	225	230	235	240
Gly	Arg	Met	Ala	Ile	Glu	Gly	Asp	Ala	Ser	Thr	Ala	Ser	Tyr	Phe	Leu	245	250	255	
Ala	Leu	Gly	Ala	Ile	Gly	Gly	Gly	Pro	Val	Arg	Val	Thr	Gly	Val	Gly	260	265	270	
Glu	Asp	Ser	Ile	Gln	Gly	Asp	Val	Ala	Phe	Ala	Ala	Thr	Leu	Ala	Ala	275	280	285	
Met	Gly	Ala	Asp	Val	Arg	Tyr	Gly	Pro	Gly	Trp	Ile	Glu	Thr	Arg	Gly	290	295	300	
Val	Arg	Val	Ala	Glu	Gly	Gly	Arg	Leu	Lys	Ala	Phe	Asp	Ala	Asp	Phe	305	310	315	320
Asn	Leu	Ile	Pro	Asp	Ala	Ala	Met	Thr	Ala	Ala	Thr	Leu	Ala	Leu	Tyr	325	330	335	
Ala	Asp	Gly	Pro	Cys	Arg	Leu	Arg	Asn	Ile	Gly	Ser	Trp	Arg	Val	Lys	340	345	350	
Glu	Thr	Asp	Arg	Ile	His	Ala	Met	His	Thr	Glu	Leu	Glu	Lys	Leu	Gly	355	360	365	
Ala	Gly	Val	Gln	Ser	Gly	Ala	Asp	Trp	Leu	Glu	Val	Ala	Pro	Pro	Glu	370	375	380	
Pro	Gly	Gly	Trp	Arg	Asp	Ala	His	Ile	Gly	Thr	Trp	Asp	Asp	His	Arg	385	390	395	400

Met Ala Met Cys Phe Leu Leu Ala Ala Phe Gly Pro Ala Ala Val Arg
405 410 415

Ile Leu Asp Pro Gly Cys Val Ser Lys Thr Phe Pro Asp Tyr Phe Asp
420 425 430

Val Tyr Ala Gly Leu Leu Ala Ala Arg Asp
435 440

<210> 65
<211> 427
<212> PRT
<213> Salmonella typhimurium

<400> 65

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
20 25 30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
65 70 75 80

Pro Leu Arg Ala Ser Gly Thr Leu Glu Leu Phe Leu Gly Asn Ala Gly
85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Gln Asn Glu
100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
145 150 155 160

Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175

Leu Met Thr Ala Pro Leu Ala Pro Glu Asp Thr Ile Ile Arg Val Lys
180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
195 200 205

Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
210 215 220

Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
 225 230 235 240
 Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Gly Ile Lys
 245 250 255
 Gly Gly Thr Val Lys Val Thr Gly Ile Gly Gly Lys Ser Met Gln Gly
 260 265 270
 Asp Ile Arg Phe Ala Asp Val Leu His Lys Met Gly Ala Thr Ile Thr
 275 280 285
 Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
 290 295 300
 Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
 305 310 315 320
 Thr Ala Leu Phe Ala Lys Gly Thr Thr Thr Leu Arg Asn Ile Tyr Asn
 325 330 335
 Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
 340 345 350
 Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
 355 360 365
 Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
 370 375 380
 His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400
 Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415
 Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
 420 425

<210> 66
 <211> 1894
 <212> DNA
 <213> Synechocystis sp.

<220>
 <221> CDS
 <222> (275)..(1618)

<400> 66
 acgggctgta acggtagtag ggggtcccgag cacaaaagcg gtgccggcaa gcagaactaa 60
 tttccatggg gaataatggt atttcattgg ttggcctct ggtctggcaa tggttgctag 120
 gcgatcgctt gttgaaatta acaaactgtc gcccttcac tgaccatggt aacgatgttt 180
 ttacttcct tgactaaccg aggaaaattt ggcggggggc agaaatgcca atacaattta 240

gcttggtctt ccctgcccct aatttgctccc ctcc atg gcc ttg ctt tcc ctc aac	295
Met Ala Leu Leu Ser Leu Asn	
1 5	
aat cat caa tcc cat caa cgc tta act gtt aat ccc cct gcc caa ggg	343
Asn His Gln Ser His Gln Arg Leu Thr Val Asn Pro Pro Ala Gln Gly	
10 15 20	
gtc gct ttg act ggc cgc cta agg gtg ccg ggg gat aaa tcc att tcc	391
Val Ala Leu Thr Gly Arg Leu Arg Val Pro Gly Asp Lys Ser Ile Ser	
25 30 35	
cat cgg gcc ttg atg ttg ggg gcg atc gcc acc ggg gaa acc att atc	439
His Arg Ala Leu Met Leu Gly Ala Ile Ala Thr Gly Glu Thr Ile Ile	
40 45 50 55	
gaa ggg cta ctg ttg ggg gaa gat ccc cgt agt acg gcc cat tgc ttt	487
Glu Gly Leu Leu Leu Gly Glu Asp Pro Arg Ser Thr Ala His Cys Phe	
60 65 70	
cgg gcc atg gga gca gaa atc agc gaa cta aat tca gaa aaa atc atc	535
Arg Ala Met Gly Ala Glu Ile Ser Glu Leu Asn Ser Glu Lys Ile Ile	
75 80 85	
gtt cag ggt cgg ggt ctg gga cag ttg cag gaa ccc agt acc gtt ttg	583
Val Gln Gly Arg Gly Leu Gly Gln Leu Gln Glu Pro Ser Thr Val Leu	
90 95 100	
gat gcg ggg aac tct ggc acc acc atg cgc tta atg ttg ggc ttg cta	631
Asp Ala Gly Asn Ser Gly Thr Thr Met Arg Leu Met Leu Gly Leu Leu	
105 110 115	
gcc ggg caa aaa gat tgt tta ttc acc gtc acc ggc gat gat tcc ctc	679
Ala Gly Gln Lys Asp Cys Leu Phe Thr Val Thr Gly Asp Asp Ser Leu	
120 125 130 135	
cgt cac cgc ccc atg tcc cgg gta att caa ccc ttg caa caa atg ggg	727
Arg His Arg Pro Met Ser Arg Val Ile Gln Pro Leu Gln Gln Met Gly	
140 145 150	
gca aaa att tgg gcc cgg agt aac ggc aag ttt gcg ccg ctg gca gtc	775
Ala Lys Ile Trp Ala Arg Ser Asn Gly Lys Phe Ala Pro Leu Ala Val	
155 160 165	
cag ggt agc caa tta aaa ccg atc cat tac cat tcc ccc att gct tca	823
Gln Gly Ser Gln Leu Lys Pro Ile His Tyr His Ser Pro Ile Ala Ser	
170 175 180	
gcc cag gta aag tcc tgc ctg ttg cta gcg ggg tta acc acc gag ggg	871
Ala Gln Val Lys Ser Cys Leu Leu Leu Ala Gly Leu Thr Thr Glu Gly	
185 190 195	
gac acc acg gtt aca gaa cca gct cta tcc cgg gat cat agc gaa cgc	919
Asp Thr Thr Val Thr Glu Pro Ala Leu Ser Arg Asp His Ser Glu Arg	
200 205 210 215	

atg ttg cag gcc ttt gga gcc aaa tta acc att gat cca gta acc cat	967
Met Leu Gln Ala Phe Gly Ala Lys Leu Thr Ile Asp Pro Val Thr His	
220 225 230	
agc gtc act gtc cat ggc ccg gcc cat tta acg ggg caa cgg gtg gtg	1015
Ser Val Thr Val His Gly Pro Ala His Leu Thr Gly Gln Arg Val Val	
235 240 245	
gtg cca ggg gac atc agc tcg gcg gcc ttt tgg tta gtg gcg gca tcc	1063
Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu Val Ala Ala Ser	
250 255 260	
att ttg cct gga tca gaa ttg ttg gtg gaa aat gta ggc att aac ccc	1111
Ile Leu Pro Gly Ser Glu Leu Leu Val Glu Asn Val Gly Ile Asn Pro	
265 270 275	
acc agg aca ggg gtg ttg gaa gtg ttg gcc cag atg ggg gcg gac att	1159
Thr Arg Thr Gly Val Leu Glu Val Leu Ala Gln Met Gly Ala Asp Ile	
280 285 290 295	
acc ccg gag aat gaa cga ttg gta acg ggg gaa ccg gta gca gat ctg	1207
Thr Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp Leu	
300 305 310	
cgg gtt agg gca agc cat ctc cag ggt tgc acc ttc ggc ggc gaa att	1255
Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu Ile	
315 320 325	
att ccc cga ctg att gat gaa att ccc att ttg gca gtg gcg gcg gcc	1303
Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala Ala	
330 335 340	
ttt gca gag ggc act acc cgc att gaa gat gcc gca gaa ctg agg gtt	1351
Phe Ala Glu Gly Thr Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg Val	
345 350 355	
aaa gaa agc gat cgc ctg gcg gcc att gct tcg gag ttg ggc aaa atg	1399
Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys Met	
360 365 370 375	
ggg gcc aaa gtc acc gaa ttt gat gat ggc ctg gaa att caa ggg gga	1447
Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly Gly	
380 385 390	
agc ccg tta caa ggg gcc gag gtg gat agc ttg acg gat cat cgc att	1495
Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Leu Thr Asp His Arg Ile	
395 400 405	
gcc atg gcg ttg gcg atc gcc gct tta ggt agt ggg ggg caa aca att	1543
Ala Met Ala Leu Ala Ile Ala Ala Leu Gly Ser Gly Gly Gln Thr Ile	
410 415 420	
att aac cgg gcg gaa gcg gcc gcc att tcc tat cca gaa ttt ttt ggc	1591
Ile Asn Arg Ala Glu Ala Ala Ala Ile Ser Tyr Pro Glu Phe Phe Gly	
425 430 435	

acg cta ggg caa gtt gcc caa gga taa agttagaaaa actcctgggc 1638
 Thr Leu Gly Gln Val Ala Gln Gly
 440 445

ggtttgtaaa tgttttacca aggtagtttg gggtaaaggc cccagcaagt gctgccaggg 1698

taatttatcc gcaattgacc aatcggcacg gaccgtatcg ttcaaactgg gtaattctcc 1758

ctttaattcc ttaaaagctc gcttaaaact gcccaacgta tctccgtaat ggcgagtgg 1818

tagaagtaat ggggccaaac ggcgatcgcc acgggaaatt aaagcctgca tcaactgacca 1878

cttataactt tcggga 1894

<210> 67
 <211> 447
 <212> PRT
 <213> Synechocystis sp.

<400> 67

Met Ala Leu Leu Ser Leu Asn Asn His Gln Ser His Gln Arg Leu Thr
 1 5 10 15

Val Asn Pro Pro Ala Gln Gly Val Ala Leu Thr Gly Arg Leu Arg Val
 20 25 30

Pro Gly Asp Lys Ser Ile Ser His Arg Ala Leu Met Leu Gly Ala Ile
 35 40 45

Ala Thr Gly Glu Thr Ile Ile Glu Gly Leu Leu Leu Gly Glu Asp Pro
 50 55 60

Arg Ser Thr Ala His Cys Phe Arg Ala Met Gly Ala Glu Ile Ser Glu
 65 70 75 80

Leu Asn Ser Glu Lys Ile Ile Val Gln Gly Arg Gly Leu Gly Gln Leu
 85 90 95

Gln Glu Pro Ser Thr Val Leu Asp Ala Gly Asn Ser Gly Thr Thr Met
 100 105 110

Arg Leu Met Leu Gly Leu Leu Ala Gly Gln Lys Asp Cys Leu Phe Thr
 115 120 125

Val Thr Gly Asp Asp Ser Leu Arg His Arg Pro Met Ser Arg Val Ile
 130 135 140

Gln Pro Leu Gln Gln Met Gly Ala Lys Ile Trp Ala Arg Ser Asn Gly
 145 150 155 160

Lys Phe Ala Pro Leu Ala Val Gln Gly Ser Gln Leu Lys Pro Ile His
 165 170 175

Tyr His Ser Pro Ile Ala Ser Ala Gln Val Lys Ser Cys Leu Leu Leu
 180 185 190

Ala	Gly	Leu	Thr	Thr	Glu	Gly	Asp	Thr	Thr	Val	Thr	Glu	Pro	Ala	Leu	195	200	205	
Ser	Arg	Asp	His	Ser	Glu	Arg	Met	Leu	Gln	Ala	Phe	Gly	Ala	Lys	Leu	210	215	220	
Thr	Ile	Asp	Pro	Val	Thr	His	Ser	Val	Thr	Val	His	Gly	Pro	Ala	His	225	230	235	240
Leu	Thr	Gly	Gln	Arg	Val	Val	Val	Pro	Gly	Asp	Ile	Ser	Ser	Ala	Ala	245	250	255	
Phe	Trp	Leu	Val	Ala	Ala	Ser	Ile	Leu	Pro	Gly	Ser	Glu	Leu	Leu	Val	260	265	270	
Glu	Asn	Val	Gly	Ile	Asn	Pro	Thr	Arg	Thr	Gly	Val	Leu	Glu	Val	Leu	275	280	285	
Ala	Gln	Met	Gly	Ala	Asp	Ile	Thr	Pro	Glu	Asn	Glu	Arg	Leu	Val	Thr	290	295	300	
Gly	Glu	Pro	Val	Ala	Asp	Leu	Arg	Val	Arg	Ala	Ser	His	Leu	Gln	Gly	305	310	315	320
Cys	Thr	Phe	Gly	Gly	Glu	Ile	Ile	Pro	Arg	Leu	Ile	Asp	Glu	Ile	Pro	325	330	335	
Ile	Leu	Ala	Val	Ala	Ala	Ala	Phe	Ala	Glu	Gly	Thr	Thr	Arg	Ile	Glu	340	345	350	
Asp	Ala	Ala	Glu	Leu	Arg	Val	Lys	Glu	Ser	Asp	Arg	Leu	Ala	Ala	Ile	355	360	365	
Ala	Ser	Glu	Leu	Gly	Lys	Met	Gly	Ala	Lys	Val	Thr	Glu	Phe	Asp	Asp	370	375	380	
Gly	Leu	Glu	Ile	Gln	Gly	Gly	Ser	Pro	Leu	Gln	Gly	Ala	Glu	Val	Asp	385	390	395	400
Ser	Leu	Thr	Asp	His	Arg	Ile	Ala	Met	Ala	Leu	Ala	Ile	Ala	Ala	Leu	405	410	415	
Gly	Ser	Gly	Gly	Gln	Thr	Ile	Ile	Asn	Arg	Ala	Glu	Ala	Ala	Ala	Ile	420	425	430	
Ser	Tyr	Pro	Glu	Phe	Phe	Gly	Thr	Leu	Gly	Gln	Val	Ala	Gln	Gly		435	440	445	

```

<210> 68
<211> 1479
<212> DNA
<213> Dichelobacter nodosus

<220>
<221> CDS
<222> (107)..(1438)

<400> 68
tttaaaaaca atgagttaaa aaattatttt tctggcacac gcgctttttt tgcatttttt      60

ctcccatttt tccggcacaa taacgttggg ttataaaaag gaaatg atg atg acg      115
                                   Met Met Thr
                                   1

aat ata tgg cac acc gcg ccc gtc tct gcg ctt tcc ggc gaa ata acg      163
Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr
   5                               10                               15

ata tgc ggc gat aaa tca atg tcg cat cgc gcc tta tta tta gca gcg      211
Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Leu Ala Ala
  20                               25                               30                               35

tta gca gaa gga caa acg gaa atc cgc ggc ttt tta gcg tgc gcg gat      259
Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp
                40                               45                               50

tgt ttg gcg acg cgg caa gca ttg cgc gca tta ggc gtt gat att caa      307
Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln
                55                               60                               65

aga gaa aaa gaa ata gtg acg att cgc ggt gtg gga ttt ctg ggt ttg      355
Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu
                70                               75                               80

cag ccg ccg aaa gca ccg tta aat atg caa aac agt ggc act agc atg      403
Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly Thr Ser Met
                85                               90                               95

cgt tta ttg gca gga att ttg gca gcg cag cgc ttt gag agc gtg tta      451
Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu
  100                               105                               110                               115

tgc ggc gat gaa tca tta gaa aaa cgt ccg atg cag cgc att att acg      499
Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr
                120                               125                               130

ccg ctt gtg caa atg ggg gca aaa att gtc agt cac agc aat ttt acg      547
Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr
                135                               140                               145

gcg ccg tta cat att tca gga cgc ccg ctg acc ggc att gat tac gcg      595
Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala
                150                               155                               160

tta ccg ctt ccc agc gcg caa tta aaa agt tgc ctt att ttg gca gga      643

```

Leu	Pro	Leu	Pro	Ser	Ala	Gln	Leu	Lys	Ser	Cys	Leu	Ile	Leu	Ala	Gly		
165						170					175						
tta	ttg	gct	gac	ggc	acc	acg	cgg	ctg	cat	act	tgc	ggc	atc	agt	cgc	691	
Leu	Leu	Ala	Asp	Gly	Thr	Thr	Arg	Leu	His	Thr	Cys	Gly	Ile	Ser	Arg		
180					185					190					195		
gac	cac	acg	gaa	cgc	atg	ttg	ccg	ctt	ttt	ggc	ggc	gca	ctt	gag	atc	739	
Asp	His	Thr	Glu	Arg	Met	Leu	Pro	Leu	Phe	Gly	Gly	Ala	Leu	Glu	Ile		
				200					205					210			
aag	aaa	gag	caa	ata	atc	gtc	acc	ggc	gga	caa	aaa	ttg	cac	ggc	tgc	787	
Lys	Lys	Glu	Gln	Ile	Ile	Val	Thr	Gly	Gly	Gln	Lys	Leu	His	Gly	Cys		
			215					220					225				
gtg	ctt	gat	att	gtc	ggc	gat	ttg	tcg	gcg	gcg	gcg	ttt	ttt	atg	gtt	835	
Val	Leu	Asp	Ile	Val	Gly	Asp	Leu	Ser	Ala	Ala	Ala	Phe	Phe	Met	Val		
		230					235						240				
gcg	gct	ttg	att	gcg	ccg	cgc	gcg	gaa	gtc	gtt	att	cgt	aat	gtc	ggc	883	
Ala	Ala	Leu	Ile	Ala	Pro	Arg	Ala	Glu	Val	Val	Ile	Arg	Asn	Val	Gly		
		245				250					255						
att	aat	ccg	acg	cgg	gcg	gca	atc	att	act	ttg	ttg	caa	aaa	atg	ggc	931	
Ile	Asn	Pro	Thr	Arg	Ala	Ala	Ile	Ile	Thr	Leu	Leu	Gln	Lys	Met	Gly		
260					265				270					275			
gga	cgg	att	gaa	ttg	cat	cat	cag	cgc	ttt	tgg	ggc	gcc	gaa	ccg	gtg	979	
Gly	Arg	Ile	Glu	Leu	His	His	Gln	Arg	Phe	Trp	Gly	Ala	Glu	Pro	Val		
			280					285						290			
gca	gat	att	gtt	gtt	tat	cat	tca	aaa	ttg	cgc	ggc	att	acg	gtg	gcg	1027	
Ala	Asp	Ile	Val	Val	Tyr	His	Ser	Lys	Leu	Arg	Gly	Ile	Thr	Val	Ala		
			295					300					305				
ccg	gaa	tgg	att	gcc	aac	gcg	att	gat	gaa	ttg	ccg	att	ttt	ttt	att	1075	
Pro	Glu	Trp	Ile	Ala	Asn	Ala	Ile	Asp	Glu	Leu	Pro	Ile	Phe	Phe	Ile		
		310					315					320					
gcg	gca	gct	tgc	gcg	gaa	ggg	acg	act	ttt	gtg	ggc	aat	ttg	tca	gaa	1123	
Ala	Ala	Ala	Cys	Ala	Glu	Gly	Thr	Thr	Phe	Val	Gly	Asn	Leu	Ser	Glu		
		325				330					335						
ttg	cgt	gtg	aaa	gaa	tcg	gat	cgt	tta	gcg	gcg	atg	gcg	caa	aat	tta	1171	
Leu	Arg	Val	Lys	Glu	Ser	Asp	Arg	Leu	Ala	Ala	Met	Ala	Gln	Asn	Leu		
340					345				350					355			
caa	act	ttg	ggc	gtg	gcg	tgc	gac	gtt	ggc	gcc	gat	ttt	att	cat	ata	1219	
Gln	Thr	Leu	Gly	Val	Ala	Cys	Asp	Val	Gly	Ala	Asp	Phe	Ile	His	Ile		
				360				365						370			
tat	gga	aga	agc	gat	cgg	caa	ttt	tta	ccg	gcg	cgg	gtg	aac	agt	ttt	1267	
Tyr	Gly	Arg	Ser	Asp	Arg	Gln	Phe	Leu	Pro	Ala	Arg	Val	Asn	Ser	Phe		
			375				380						385				
ggc	gat	cat	cgg	att	gcg	atg	agt	ttg	gcg	gtg	gca	ggc	gtg	cgc	gcg	1315	
Gly	Asp	His	Arg	Ile	Ala	Met	Ser	Leu	Ala	Val	Ala	Gly	Val	Arg	Ala		

390	395	400	
gca ggt gaa tta ttg att gat gac ggc gcg gtg gcg gcg gtt tct atg			1363
Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala Val Ser Met			
405	410	415	
ccg caa ttt cgc gat ttt gcc gcc gca att ggt atg aat gta gga gaa			1411
Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn Val Gly Glu			
420	425	430	435
aaa gat gcg aaa aat tgt cac gat tga tggtcctagc ggtgttgga			1458
Lys Asp Ala Lys Asn Cys His Asp			
440			
aaggcacggt ggcgcaagct t			1479
<210> 69			
<211> 443			
<212> PRT			
<213> Dichelobacter nodosus			
<400> 69			
Met Met Thr Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly			
1	5	10	15
Glu Ile Thr Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu			
20	25	30	
Leu Ala Ala Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala			
35	40	45	
Cys Ala Asp Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val			
50	55	60	
Asp Ile Gln Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe			
65	70	75	80
Leu Gly Leu Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly			
85	90	95	
Thr Ser Met Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu			
100	105	110	
Ser Val Leu Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg			
115	120	125	
Ile Ile Thr Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser			
130	135	140	
Asn Phe Thr Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile			
145	150	155	160
Asp Tyr Ala Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile			
165	170	175	

Leu Ala Gly Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly
 180 185 190
 Ile Ser Arg Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala
 195 200 205
 Leu Glu Ile Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu
 210 215 220
 His Gly Cys Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe
 225 230 235 240
 Phe Met Val Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg
 245 250 255
 Asn Val Gly Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln
 260 265 270
 Lys Met Gly Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala
 275 280 285
 Glu Pro Val Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile
 290 295 300
 Thr Val Ala Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile
 305 310 315 320
 Phe Phe Ile Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn
 325 330 335
 Leu Ser Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala
 340 345 350
 Gln Asn Leu Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe
 355 360 365
 Ile His Ile Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val
 370 375 380
 Asn Ser Phe Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly
 385 390 395 400
 Val Arg Ala Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala
 405 410 415
 Val Ser Met Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn
 420 425 430
 Val Gly Glu Lys Asp Ala Lys Asn Cys His Asp
 435 440

<U>
 <210> 70
 <211> 455
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Synthetic

 <400> 70

 Met Leu His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
 1 5 10 15

 Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
 20 25 30

 Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
 35 40 45

 Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
 50 55 60

 Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
 65 70 75 80

 Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
 85 90 95

 Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
 100 105 110

 Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
 115 120 125

 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
 130 135 140

 Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
 145 150 155 160

 Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
 165 170 175

 Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
 180 185 190

 Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
 195 200 205

 Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
 210 215 220

 Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
 225 230 235 240

Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
 245 250 255
 Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
 260 265 270
 Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
 275 280 285
 Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
 290 295 300
 Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
 305 310 315 320
 Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
 325 330 335
 Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
 340 345 350
 Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
 355 360 365
 Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
 370 375 380
 Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
 385 390 395 400
 His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
 405 410 415
 Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
 420 425 430
 Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
 435 440 445
 Leu Ser Asp Thr Lys Ala Ala
 450 455

</U>